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(54) Title: CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO INFECTIOUS DISEASE

(57) Abstract: Host nucleic acids and host proteins that participate in viral infection, such as human immunodeficiency virus (HIV), influenza A, and Ebola virus, have been identified. Interfering with or disrupting the interaction between a host nucleic acid or host protein and a virus or viral protein confers an inhibition of or resistance to infection. Thus, interfering with such an interaction in a host subject can confer a therapeutic or prophylactic effect against a virus. The sequences identified can be used to identify agents that reduce or inhibit viral infection.

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**CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO
INFECTIOUS DISEASE**

CROSS REFERENCE TO RELATED APPLICATIONS

- 5 This application claims the benefit of U.S. Provisional Application Nos. 60/427,464 filed November 18, 2002 and 60/482,604 filed June 25, 2003, both herein incorporated by reference.

FIELD

- 10 The present disclosure relates to host nucleic acid sequences, and proteins encoded by these sequences, that are involved in viral infection or are otherwise associated with the life cycle of a virus. Decreasing or inhibiting the interaction of these host sequences with a viral sequence can be used to decrease or inhibit infection by the virus.

BACKGROUND

- 15 Infectious diseases affect the health of people and animals around the world, causing serious illness and death. Public health efforts have focused on behavioral modification and other public health efforts to reduce the incidences of infection, while treatment regimens for these diseases have focused on pharmaceuticals, such as antibiotics and anti-viral medications. However, educating people about modifying behavior can be difficult, and that approach alone rarely can significantly
20 diminish the incidence of infection. Furthermore, modifying the behavior of domestic or wild animals would not result in diminished infections. Stopping the spread of infections in an animal population typically involves wholesale slaughter. Few vaccines are available or wholly effective, and they tend to be specific for particular conditions.

- 25 The rate of HIV (human immunodeficiency virus) infection is increasing. HIV and its associated acquired immune deficiency syndrome (AIDS) accounted for approximately 5% of all deaths in the United States in the year 2000, while over 313,000 persons were reported to be living with AIDS in that same year. Centers for Disease Control and Prevention, *HIV/AIDS Surveillance Supplemental Report*, 8(1):1-22 (2002). These increasing infection rates have occurred, even though
30 the mode of HIV infection has been known for almost 20 years, and educational programs around the world have promoted behavioral modifications meant to reduce HIV infection. Incidence and death rates due to HIV disease have been decreasing since the mid-90's, in part due to aggressive antiviral therapies, which frequently have toxic side effects and strict dosage schedules. However, even with treatment, the patient is not cured of the disease, and to date, no effective vaccine therapy has been found.

- 35 In other diseases, such as infection by the Ebola virus, not only are treatments limited, but containment or prevention of infections is difficult because the life cycle of the virus is not well known. The natural reservoir for the Ebola virus, that is the place or population in nature where the virus resides between human outbreaks, has not yet been identified.

Additionally, different viral strains can rapidly evolve in response to drug usage, producing drug-resistant strains. For example, strains of the influenza virus resistant to amantadine and rimantadine have recently arisen. A recent study of 80 newly-infected people conducted by the AIDS Research Center at Rockefeller University in New York, found that as many as 16.3% of these individuals had strains of HIV associated with resistance to some treatments, and 3.8% appeared to be resistant to several currently available anti-HIV drugs. Thus, a need exists for alternative treatments for infectious disease and methods of designing new drugs to combat infectious disease.

SUMMARY

Several host nucleic acid sequences involved in viral infection have been identified using gene trap methods. The identification of these host sequences and their encoded products permits the identification of sequences that can be targeted for therapeutic intervention.

The disclosed host sequences (including the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby (such as SEQ ID NOS: 228, 230, and 232), as well as variants, fusions, and fragments thereof that retain the appropriate biological activity) can mediate infection, and in some examples these host nucleic acids are required for infection. For example, the host nucleic acid can encode a cellular receptor or ligand or a fragment thereof that is recognized by a virus, such as the T-cell V-D-J beta 2.1 chain. In another example, the host nucleic acid encodes an enzyme that mediates viral infection, such as the β -chimerin rho-GTPase (referred to herein as β -chimerin). In another example, the host nucleic acid encodes a Ras oncogene family member such as Rab9. It is demonstrated herein that Rab9 is a host protein involved in infection by pathogens (such as viruses and bacteria) that use similar pathways for morphogenesis of infectious particles. In particular examples, Rab9 is involved in infection by pathogens (such as viruses and bacteria) that utilize lipid rafts. Thus, for example, interfering with the interaction between the disclosed host proteins and a viral or pathogen protein, for example by disrupting the expression of the host nucleic acid within a host cell, or by administering an agent that decreases binding between a host protein and a viral protein, can inhibit, or even prevent, infection of that host cell by the associated virus. Moreover, the identification of particular host enzymes or other host proteins involved in infection provides a method for developing new therapies targeted at inhibiting infection, at the protein or nucleic acid level.

In some examples, the nucleic acid itself mediates viral infection. For example, the nucleotide sequence of a host nucleic acid in the host genome can be recognized by the virus during integration of the viral genome into the host genome. The identification of nucleic acid sequences that are involved in the pathogenesis of infection therefore provides an important tool for interfering with infection.

This genomics-based discovery of nucleic acids and proteins involved in, or even required for, infection provides a new paradigm for identifying and validating various aspects of infectious disease, including assessing individual or population resistance to infection and finding novel

diagnostic and drug targets for infectious disease and altering the nucleotide sequence of the host nucleic acid.

Based on the identification of several host nucleic acid and protein sequences involved in viral infection, provided herein are methods for decreasing infection of a host cell by a virus, such as HIV, Ebola, or influenza A, or treating such a viral infection, by interfering with the activity or expression of one or more host proteins shown in Table 1 (including the target sequences associated with any of SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof), such as at least two host proteins, or at least three host proteins. Also provided are methods for identifying agents that can decrease viral infection of a host cell, such as infection by HIV, Ebola, or influenza A. In addition, cells and non-human mammals are provided that have decreased susceptibility to viral infection, such as HIV, Ebola, or influenza A infection.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a schematic illustration of the U3neoSV1 retroviral vector, which is capable of isolating the nucleic acids described herein using the gene-trap method.

FIG. 2 is a schematic illustration of the gene-trap method.

FIG. 3 is a schematic illustration of one method of identifying host genes described herein.

FIG. 4 is a flow chart illustrating a method for isolating cells resistant to HIV infection, including HIV-1 and HIV-2 infection.

FIG. 5 is a bar graph showing the relative amount of p24 in HIV-infected cells in the presence of various siRNAs. CHN (β -chimerin); KOX (similar to KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); RAB (Rab9); KIAA1259; F3 (tissue factor 3; thromboplastin); AXL (AXL receptor tyrosine kinase); Mslb (mammalian selenium binding protein).

FIG. 6 is a schematic drawing showing a model of Rab9 involvement in lipid raft formation.

SEQUENCE LISTING

The nucleotide sequences of the nucleic acids described herein are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. Additionally, the nucleic acid sequences shown in SEQ ID NOS: 1-226 inherently disclose the corresponding polypeptide sequences of coding sequences (resulting translations of the nucleotide sequences), even when those polypeptide sequences are not explicitly provided herein.

SEQ ID NO: 1 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E8, entire insert. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor V beta chain (T-cell receptor beta). Further information on the T-cell receptor V beta chain can be found in WO 01/23409, WO 01/55302, WO 01/57182, and WO 01/94629.

SEQ ID NO: 2 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, distal end. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor V beta chain.

5 SEQ ID NO: 3 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 4 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, distal end. The human homolog is the (+) strand of GenBank Accession No. AC00616.7, T-cell receptor beta.

10 SEQ ID NO: 5 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor beta.

SEQ ID NO: 6 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

15 SEQ ID NO: 7 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 18E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

20 SEQ ID NO: 8 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 9 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 2E22, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC099395.2, T-cell receptor beta.

25 SEQ ID NO: 10 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

30 SEQ ID NO: 11 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 12 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, distal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

35 SEQ ID NO: 13 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 14 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 15 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, distal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

5 SEQ ID NO: 16 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 17 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

10 SEQ ID NO: 18 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 19 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

15 SEQ ID NO: 20 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BD, proximal end. The human homolog is the (+) strand of GenBank Accession No. M16834.1, T-cell receptor V-D-J-beta 2.1 chain (described in WO 02/057414 and Reynolds *et al.*, *Cell* 50(1):107-17, 1987).

20 SEQ ID NO: 21 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, distal end. The human homolog is the (-) strand of GenBank Accession No. AC004593.1 including beta-chimaerin rho GTPase (CHN2) (for example see WO 01/12659).

25 SEQ ID NO: 22 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, proximal end. The human homologs are the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta; and the (+) strand of GenBank Accession No. AC004593.1 including beta-chimaerin (CHN2).

30 SEQ ID NO: 23 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AL049699.8, including malic enzyme 1 (ME1) NADP(+)-dependent cytosolic. Further information on this gene can be found in WO 01/55301 and WO 01/53312.

35 SEQ ID NO: 24 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18BD, distal end. The human homolog is the (+) strand of GenBank Accession No. AC123903.1, including hypothetical protein XP_174419.

SEQ ID NO: 25 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, distal end. The human

homolog is the (+) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 26 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, middle of insert. The human
5 homolog is the (+) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 27 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, proximal end. The human
10 homologs are the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta; and (-) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 28 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, distal end. The human homolog is the (-) strand of GenBank Accession No. M26920.1, alpha satellite DNA.

SEQ ID NO: 29 is a nucleic acid sequence associated with viral, such as HIV, infection, and
15 is the clone identified as Nucleotide Sequence 2E22, distal end. The human homologs are the (+) strand of GenBank Accession No. AP004369.3, including LOC253788 (and neighboring similar to RIKEN cDNA 1700001L23 (LOC219938)); and the (+) strand of GenBank Accession No. AC093117.2, between coagulation factor III, thromboplastin, tissue factor (F3) and LOC91759.

SEQ ID NO: 30 is a nucleic acid sequence associated with viral, such as HIV, infection, and
20 is the clone identified as Nucleotide Sequence 2B13, distal end. The human homolog is the (-) strand of GenBank Accession No. AC092043.2, between similar to zinc finger protein 7 KOX4 (LOC131880) and LOC166140.

SEQ ID NO: 31 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, distal end. The human homologs are the (-)
25 strand of GenBank Accession No. AL136963.17, between LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); and the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 32 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, distal end. The human homolog is the (-) strand
30 of GenBank Accession No. AL133293.28, between ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC).

SEQ ID NO: 33 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, distal end. The human homolog is the (-) strand of GenBank Accession No. AL161417.17, KIAA0564.

35 SEQ ID NO: 34 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, distal end. The human homologs are the (-) strand of GenBank Accession No. Z12006.1, alpha satellite DNA; and the (+) and (-) strands of GenBank Accession No. AC093577.2, M96 protein.

SEQ ID NO: 35 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, distal end. The human homologs are the (-) strand of GenBank Accession No. Z78022.1, hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); and the (+) strand of GenBank Accession No. AL136220.14, between
5 LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2).

SEQ ID NO: 36 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3B1, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

10 SEQ ID NO: 37 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5B5, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

15 SEQ ID NO: 38 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

20 SEQ ID NO: 39 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

25 SEQ ID NO: 40 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

30 SEQ ID NO: 41 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

35 SEQ ID NO: 42 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 43 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E3, entire insert. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 44 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E5, proximal end. The human

homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 45 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6B1, entire insert. The human
5 homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 46 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing
10 preferred translocation partner in lipoma (LPP).

SEQ ID NO: 47 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

15 SEQ ID NO: 48 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 49 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC104036.8, between LOC253121 and hyaluronan synthase 2 (HAS2).
20

SEQ ID NO: 50 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E1, proximal end. The human
25 homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3 (see WO 01/57270, WO 01/57271, WO 01/57273, WO 01/57274, WO 01/57275, WO 01/57276, WO 01/57277, WO 01/57278, or Tatarelli *et al.*, *Genomics* 68(1):1-12, 2000).

SEQ ID NO: 51 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.
30

SEQ ID NO: 52 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 53 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.
35

SEQ ID NO: 54 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 55 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

5 SEQ ID NO: 56 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 57 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

10 SEQ ID NO: 58 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 (see Watanabe *et al.*, *Jpn. J. Cancer Res.* 93:1114-22, 2002).

15 SEQ ID NO: 59 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1.

20 SEQ ID NO: 60 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, distal end. The human homolog is the (+) strand of GenBank Accession No. AL445675.9, between LOC149360 and LOC253961.

SEQ ID NO: 61 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL391986.12, between KIAA1560 and Tectorin beta (TECTB).

25 SEQ ID NO: 62 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AC016826.9, including Cadherin related 23 (CDH23).

30 SEQ ID NO: 63 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AL357372.12, Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10).

35 SEQ ID NO: 64 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between exportin 5 (XPO5) and DNA polymerase eta (POLH).

SEQ ID NO: 65 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

SEQ ID NO: 66 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1E, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

5 SEQ ID NO: 67 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including heterogenous nuclear riboprotein C (C1/C2) (HNRPC).

10 SEQ ID NO: 68 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 69 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

15 SEQ ID NO: 70 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 71 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

20 SEQ ID NO: 72 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

25 SEQ ID NO: 73 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B21, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 74 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B25, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

30 SEQ ID NO: 75 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

35 SEQ ID NO: 76 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AL050324.5, including alpha-endosulfine pseudogene (ENSAP) and LOC128741.

SEQ ID NO: 77 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AC017060.7, including LOC222888.

SEQ ID NO: 78 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, distal end. The human homolog is the (+) strand of GenBank Accession No. AL161731.20, between LOC138421 and zinc finger protein 297B (ZNF297B).

5 SEQ ID NO: 79 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, distal end. The human homolog is the (-) strand of GenBank Accession No. AC012366.10, including sideroflexin 5 (SFXN5).

10 SEQ ID NO: 80 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, distal end. The human homolog is the (+) strand of GenBank Accession No. AL645504.10, including importin 9 (FLJ10402).

SEQ ID NO: 81 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence GV1-1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

15 SEQ ID NO: 82 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence GV1-1B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 83 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

20 SEQ ID NO: 84 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

25 SEQ ID NO: 85 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 86 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

30 SEQ ID NO: 87 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 88 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

35 SEQ ID NO: 89 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 90 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

5 SEQ ID NO: 91 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 92 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

10 SEQ ID NO: 93 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 94 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-B1, distal end. The human homolog is the (+) and (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

15 SEQ ID NO: 95 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 96 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 97 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

25 SEQ ID NO: 98 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 99 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

30 SEQ ID NO: 100 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

35 SEQ ID NO: 101 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

SEQ ID NO: 102 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, distal end. The human homolog is the

(+) and (-) strands of GenBank Accession No. AC107081.5, copper metabolism gene (MURR1) and chaperonin containing TCP1, subunit 4 (CCT4).

SEQ ID NO: 103 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (-)
5) strand of GenBank Accession No. AC099785.2, hypothetical protein FLJ40773 and similar to ribosomal protein L24-like (LOC149360).

SEQ ID NO: 104 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

10 SEQ ID NO: 105 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 106 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).
15

SEQ ID NO: 107 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 108 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B2, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC105934.2, polybromo 1 (PB1).
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SEQ ID NO: 109 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC022506.38, between DNA damage inducible transcript 3 (DDIT3) and KIAA1887.
25

SEQ ID NO: 110 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL157834.12, PDZ and LIM domain 1 (elfin) (PDLIM1).

SEQ ID NO: 111 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AL110115.38, LOC284803.
30

SEQ ID NO: 112 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL110115.38, signal peptide peptidase (HM13) and
35 LOC284803.

SEQ ID NO: 113 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL117341.26, containing PRO0097 and adjacent to FLJ31958.

SEQ ID NO: 114 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1).

- 5 SEQ ID NO: 115 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP002076.3, containing SCYE1.

- 10 SEQ ID NO: 116 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, containing SCYE1.

SEQ ID NO: 117 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC132812.9, between E3 ubiquitin ligase (SMURF2) and hypothetical protein MGC40489.

- 15 SEQ ID NO: 118 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

- 20 SEQ ID NO: 119 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

SEQ ID NO: 120 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL132989.5, between PRO1617 and retinoblastoma binding protein 1 (RBBP1).

- 25 SEQ ID NO: 121 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, RBBP1.

- 30 SEQ ID NO: 122 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, retinoblastoma binding protein 1 (RBBP1).

SEQ ID NO: 123 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC096669.1, a region of chromosome 2q12.

- 35 SEQ ID NO: 124 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, distal end. The human homolog is the (-) strands of GenBank Accession No. AF196968.4, elongation factor for selenoprotein translation (SELB).

SEQ ID NO: 125 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

5 SEQ ID NO: 126 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 127 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

10 SEQ ID NO: 128 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 129 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

15 SEQ ID NO: 130 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 131 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

20 SEQ ID NO: 132 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

25 SEQ ID NO: 133 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 134 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

30 SEQ ID NO: 135 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 136 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

35 SEQ ID NO: 137 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 138 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AL031293.1, KIAA1026.

5 SEQ ID NO: 139 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035587.5, trinucleotide repeat containing 5 (TNRC5).

 SEQ ID NO: 140 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC126182.2, homogentisate 1,2-dioxygenase (HGD).

10 SEQ ID NO: 141 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AL591643.4, a region of chromosome Xq23-24.

 SEQ ID NO: 142 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC113603.3, a region of chromosome 4p15.3.

15 SEQ ID NO: 143 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011995.8, similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883).

20 SEQ ID NO: 144 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084208.5, a region of chromosome 2q21.

 SEQ ID NO: 145 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL391259.15, a region of chromosome Xp11.4, including ubiquitin specific protease 9 (USP9X).

25 SEQ ID NO: 146 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, distal end. The human homolog is the (+) strand of GenBank Accession No. AC006397.1, LOC221829.

30 SEQ ID NO: 147 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, distal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

 SEQ ID NO: 148 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, proximal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

35 SEQ ID NO: 149 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 150 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

5 SEQ ID NO: 151 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 152 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

10 SEQ ID NO: 153 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 154 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

15 SEQ ID NO: 155 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, integrin, beta 1 (ITGB1).

20 SEQ ID NO: 156 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 157 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, ITGB1.

25 SEQ ID NO: 158 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

30 SEQ ID NO: 159 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AP001132.4, acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1).

SEQ ID NO: 160 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, distal end. The human homolog is the (-) strand of GenBank Accession No. AK025453.1, prospero-related homeobox 1 (PROX1).

35 SEQ ID NO: 161 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 162 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

5 SEQ ID NO: 163 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 164 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

10 SEQ ID NO: 165 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

15 SEQ ID NO: 166 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 167 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

20 SEQ ID NO: 168 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

25 SEQ ID NO: 169 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 170 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

30 SEQ ID NO: 171 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

35 SEQ ID NO: 172 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 173 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 174 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105001.3, between PIN2-interacting protein 1 (PINX1) and SRY (sex-determining region Y)-box7 (SOX7).

- 5 SEQ ID NO: 175 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC009520.16, LOC131920.

- 10 SEQ ID NO: 176 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL596329.5, a region of chromosome 13q14.

SEQ ID NO: 177 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC023844.6, neurotrophic tyrosine kinase, receptor, type 3 (NTRK3).

- 15 SEQ ID NO: 178 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC024940.39, between TERA protein (TERA) and hypothetical protein FLJ13224.

- 20 SEQ ID NO: 179 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC024940.39, flanking TERA protein (TERA) and hypothetical protein FLJ13224.

- 25 SEQ ID NO: 180 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084335.6, hypothetical gene LOC284260.

SEQ ID NO: 181 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

- 30 SEQ ID NO: 182 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

- 35 SEQ ID NO: 183 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC087650.12, between DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064).

SEQ ID NO: 184 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, distal end. The human homolog is the

(-) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 185 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 186 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 187 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E3, distal end. The murine homolog is the (+) strand of GenBank Accession No. NG_001440.1, *Mus musculus* 5S rRNA pseudogene (Rn5s-ps1).

SEQ ID NO: 188 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2).

SEQ ID NO: 189 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 190 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 191 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 192 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 193 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP000711.4, Down's syndrome cell adhesion molecule like 1 (DSCAML1).

SEQ ID NO: 194 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL391555.19, LOC148529.

SEQ ID NO: 195 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B4, distal end. The human homolog is the

(-) strand of GenBank Accession No. AC112129.4, Huntingtin-associated protein interacting protein (HAPIP).

5 SEQ ID NO: 196 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

10 SEQ ID NO: 197 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 198 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

15 SEQ ID NO: 199 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

20 SEQ ID NO: 200 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

25 SEQ ID NO: 201 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 202 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

30 SEQ ID NO: 203 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 204 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

35 SEQ ID NO: 205 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC005284.1, LOC350411.

SEQ ID NO: 206 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E9, proximal end. The human homolog is

the (+) strand of GenBank Accession No. AP000505.1, between allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2).

SEQ ID NO: 207 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E1, distal end. The human homolog is the
5 (-) strand of GenBank Accession No. AC008755.8, C19orf7.

SEQ ID NO: 208 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 209 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E2, proximal end. The human homolog is
10 the (-) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 210 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079030.13, a region of chromosome 12q21.

SEQ ID NO: 211 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, proximal end. The human homolog is
15 the (-) strand of GenBank Accession No. AC139138.2, between LOC339248 and hypothetical protein FLJ22659.

SEQ ID NO: 212 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E4, distal end. The human homolog is the
20 (-) strand of GenBank Accession No. AL513550.9, between SR rich protein DKFZp564B0769 and hypothetical protein MGC14793.

SEQ ID NO: 213 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, distal end. The human homolog is the
25 (-) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 214 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 215 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B3, distal end. The human homolog is the
30 (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 216 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B3, proximal end. The human homolog is
35 the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 217 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI
5 membrane anchor, (semaphoring) 7A.

SEQ ID NO: 218 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane
10 anchor, (semaphoring) 7A.

SEQ ID NO: 219 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).

SEQ ID NO: 220 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).
15

SEQ ID NO: 221 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY).
20

SEQ ID NO: 222 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115 and ACLY.

SEQ ID NO: 223 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).
25

SEQ ID NO: 224 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E7, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC124857.2, calnexin (CANX) and (-) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).
30

SEQ ID NO: 225 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, distal end. The human homolog is the (+) strand of GenBank Accession No. AC009144.5, cyclin M2 (CNNM2).
35

SEQ ID NO: 226 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC011510.7, AXL receptor tyrosine kinase (AXL).

SEQ ID NO: 227 is a nucleic acid sequence showing GenBank Accession No. BC008947, *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 228 is an amino acid sequence encoded by SEQ ID NO: 227.

5 SEQ ID NO: 229 is a nucleic acid sequence showing GenBank Accession No. NM_018131, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 230 is an amino acid sequence encoded by SEQ ID NO: 229.

10 SEQ ID NO: 231 is a nucleic acid sequence showing GenBank Accession No. NM_013451, *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*) (FER1L3), transcript variant 1, mRNA. This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 232 is an amino acid sequence encoded by SEQ ID NO: 231.

SEQ ID NOS: 233 and 234 are exemplary complementary primers.

15 SEQ ID NOS: 235-237 are primer sequences used to sequence the shuttle clones as described in Example 2.

SEQ ID NOS: 238-241 are Rab9 siRNA sequences.

SEQ ID NOS: 242-245 are AXL receptor tyrosine kinase siRNA sequences.

SEQ ID NOS: 246-295 are beta-chimerin receptor tyrosine kinase RNAi sequences.

SEQ ID NOS: 296-345 are retinoblastoma binding protein 1 RNAi sequences.

20 SEQ ID NOS: 346-395 are *Homo sapiens* chromosome 10 open reading frame 3 RNAi sequences.

SEQ ID NOS: 396-445 are *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*), transcript variant 1 RNAi sequences.

25 SEQ ID NOS: 446-495 are *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3) RNAi sequences.

SEQ ID NOS: 496-545 are malic enzyme RNAi sequences.

SEQ ID NOS: 546-595 are cadherin related 23 RNAi sequences.

SEQ ID NOS: 596-645 are sideroflexin 5 RNAi sequences.

SEQ ID NOS: 646-695 are polybromo 1 (PB1) RNAi sequences.

30 SEQ ID NOS: 696-720 are elongation factor for selenoprotein translation RNAi sequences.

SEQ ID NOS: 721-745 are integrin, beta 1 RNAi sequences.

SEQ ID NOS: 746-795 are huntingtin interacting protein 1 RNAi sequences.

SEQ ID NOS: 796-845 are cyclin M2 RNAi sequences.

35 DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

Abbreviations and Terms

The following explanations of terms and methods are provided to better describe the present disclosure and to guide those of ordinary skill in the art in the practice of the present disclosure. The singular forms "a," "an," and "the" refer to one or more than one, unless the context clearly dictates

otherwise. For example, the term "comprising a nucleic acid" includes single or plural nucleic acids and is considered equivalent to the phrase "comprising at least one nucleic acid." The term "or" refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. For example, the phrase "a first nucleic acid or a
 5 second nucleic acid" refers to the first nucleic acid, the second nucleic acid, or a combination of both the first and second nucleic acids. As used herein, "comprises" means "includes." Thus, "comprising a promoter and an open reading frame," means "including a promoter and an open reading frame," without excluding additional elements.

Unless explained otherwise, all technical and scientific terms used herein have the same
 10 meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. The materials, methods, and examples are illustrative only and not intended to be limiting.

15 A = adenine
 C = cytosine
 DNA = deoxyribonucleic acid
 ds = double-stranded (for example, dsDNA)
 G = guanine
 20 mg = milligram
 ng = nanogram
 PCR = polymerase chain reaction
 Pu = purine
 Py = pyrimidine
 25 RNA = ribonucleic acid
 mRNA = messenger RNA
 MOI = multiplicity of infection
 siRNA = short interfering or interrupting RNA
 ss = single-stranded (for example, ssDNA)
 30 T = thymine
 T_m = melting temperature
 U = uracil
 μ g = microgram
 μ l = microliter

35

Amplification of a nucleic acid. To increase the number of copies of a nucleic acid. Several methods can be used to amplify a nucleic acid, such as polymerase chain reaction (PCR). Other examples of amplification include, but are not limited to, strand displacement amplification (U.S. Patent No: 5,744,311); transcription-free isothermal amplification (U.S. Patent No: 6,033,881);

repair chain reaction amplification (WO 90/01069); ligase chain reaction amplification (European Patent Appl. 320 308); gap filling ligase chain reaction amplification (U.S. Patent No: 5,427,930); and NASBA™ RNA transcription-free amplification (U.S. Patent No: 6,025,134).

5 The amplification products ("amplicons") can be further processed, manipulated, or characterized by electrophoresis, restriction endonuclease digestion, hybridization, nucleic acid sequencing, ligation, or other molecular biology techniques. Standard protocols can be modified. For example, PCR can be modified by using reverse transcriptase PCR (RT-PCR) to amplify RNA molecules.

10 **Antisense, Sense, and Antigene.** Antisense molecules are molecules that are specifically hybridizable or specifically complementary to either RNA or the plus strand of DNA. Sense molecules are molecules that are specifically hybridizable or specifically complementary to the minus strand of DNA. Antigene molecules are either antisense or sense molecules directed to a particular dsDNA target. These molecules can be used to interfere with gene expression.

15 Double-stranded DNA (dsDNA) has two strands, a 5' to 3' strand, referred to as the plus (+) strand, and a 3' to 5' strand (the reverse complement), referred to as the minus (-) strand. Because RNA polymerase adds nucleic acids in a 5' to 3' direction, the minus strand of the DNA serves as the template for the RNA during transcription. Thus, the RNA formed will have a sequence complementary to the minus strand and virtually identical to the plus strand, except that U is substituted for T in RNA molecules.

20 **Array.** An arrangement of biological samples or molecules, such as an arrangement of tissues, cells, or biological macromolecules (including, but not limited to, peptides or nucleic acids) in addressable locations on or in a substrate. The arrangement of molecules within the array can be regular, such as being arranged in uniform rows and columns, or irregular. The number of addressable locations within the array can vary, for example from a few (such as two or three) to more than 50, 100, 200, 500, 1000, 10,000, or more. In certain examples, the array includes one or more molecules or samples occurring on the array a plurality of times (twice or more) to provide an added feature to the array, such as redundant activity or to provide internal controls. A "microarray" is an array that is miniaturized and evaluated or analyzed using microscopy.

30 Within an array, each arrayed sample or molecule is addressable, such that its location can be reliably and consistently determined within the at least two dimensions of the array. The location or address of each sample or molecule can be assigned when it is applied to the array, and a key or guide can be provided in order to correlate each location with the appropriate target sample or molecule position. Ordered arrays can be arranged in a symmetrical grid pattern or other patterns, for example, in radially distributed lines, spiral lines, or ordered clusters. Addressable arrays can be computer readable; a computer can be programmed to correlate a particular address on the array with information about the sample at that position, such as hybridization or binding data, including signal intensity. In some exemplary computer readable formats, the individual samples or molecules in the array are arranged regularly (for example, in a Cartesian grid pattern), which can be correlated to address information by a computer.

The sample or molecule addresses on an array can assume many different shapes. For example, substantially square regions can be used as addresses within arrays, but addresses can be differently shaped, for example, substantially rectangular, triangular, oval, irregular, or another shape. The term "spot" refers generally to a localized placement of molecules, tissue or cells, and is not
5 limited to a round or substantially round region or address.

Examples of macroarrays include the Histo™-array and INSTA-blot™ lines of products available from Imgenix, Inc. (San Diego, CA) and the Max Array™ line of products available from Zymed Laboratories, Inc. (South San Francisco, CA), while exemplary microarrays include the various GeneChip® technologies and products available from Affymetrix, Inc. (Santa Clara, CA) and
10 the Hilight™, Label Star™, and Array-Ready Oligo Set lines of products available from Qiagen, Inc. (Valencia, CA).

β -chimerin. The term β -chimerin includes any β -chimerin gene, cDNA, RNA, or protein from any organism and is a β -chimerin that can function as a type of rho-GTPase. In some examples, β -chimerin is involved in viral infection.

Rho-GTPases are a family of small GTPases implicated as components of cellular signal
15 transduction cascades. Signals that pass through rho-GTPase cascades can be initiated by the activation of cell surface proteins, such as growth factors. Functions of signaling cascades mediated by rho-GTPases, include, but are not limited to, alterations in cellular morphology which are linked to processes such as immune cell function, oncogenesis, metastasis and certain diseases (Peck, *FEBS Lett.* 528:27, 2002).
20

Examples of native β -chimerin nucleic acid sequences include, but are not limited to those shown in SEQ ID NOS: 21-22 (such as a target sequence associated with SEQ ID NOS: 21-22), as well as the protein sequence encoded thereby. This cell line remains CD4⁺ after exposure to HIV 1 and HIV 2 and is resistant to HIV infection. β -chimerin also includes variants, fusions, and
25 fragments of the disclosed nucleic acid and amino acid sequences that retain β -chimerin biological activity.

Examples of β -chimerin amino acid sequences include, but are not limited to: Genbank Accession Nos: NM_004067 (mRNA) and NP_004058.1 (protein). In one example, a β -chimerin sequence includes a full-length wild-type (or native) sequence, as well as β -chimerin allelic variants,
30 variants, fragments, homologs or fusion sequences that retain the ability to function as a type of rho-GTPase. In certain examples, β -chimerin has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native β -chimerin.

cDNA (complementary DNA). A piece of DNA lacking internal, non-coding segments (introns) and transcriptional regulatory sequences. A cDNA also can contain untranslated regions
35 (UTRs) that are responsible for translational control in the corresponding RNA molecule. cDNA can be produced using various methods, such as synthesis in the laboratory by reverse transcription from messenger RNA extracted from cells.

Complementary. Complementary binding occurs when the base of one nucleic acid molecule forms a hydrogen bond the base of another nucleic acid molecule. Normally, the base

adenine (A) is complementary to thymidine (T) and uracil (U), while cytosine (C) is complementary to guanine (G). For example, the sequence 5'-ATCG-3' of one ssDNA molecule can bond to 3'-TAGC-5' of another ssDNA to form a dsDNA.

Nucleic acid molecules can be complementary to each other even without complete hydrogen-bonding of all bases of each molecule. By way of example only (and without limitation), the ssDNA: 5'-GCTTGCCAAACCTACA-3' (SEQ ID NO: 233) is considered complementary to the ssDNA 3'-CGAACGGTCTGGATGT-5' (SEQ ID NO: 234) even though there is a mismatched base pair (A-C rather than A-T or G-C) at the ninth position.

Conservative substitution: A substitution of an amino acid residue for another amino acid residue having similar biochemical properties. Typically, conservative substitutions have little to no impact on the biological activity of a resulting polypeptide. In a particular example, a conservative substitution is an amino acid substitution in a peptide that does not substantially affect the biological function of the peptide. A peptide can include one or more amino acid substitutions, for example 2-10 conservative substitutions, 2-5 conservative substitutions, 4-9 conservative substitutions, such as 2, 5 or 10 conservative substitutions.

For example, a conservative substitution in a β -chimerin peptide (such as a peptide encoded by a target sequence associated with SEQ ID NO: 21 or 22) does not substantially affect the ability of β -chimerin to confer resistance to HIV infection. In another example, a conservative substitution in a Rab9 peptide (such as a peptide encoded by a target sequence associated with SEQ ID NOS: 118 or 119) is one that does not substantially affect the ability of Rab9 to confer resistance to infection by a pathogen that can hijack a lipid raft, such as HIV or Ebola.

A polypeptide can be produced to contain one or more conservative substitutions by manipulating the nucleotide sequence that encodes that polypeptide using, for example, standard procedures such as site-directed mutagenesis or PCR. Alternatively, a polypeptide can be produced to contain one or more conservative substitutions by using standard peptide synthesis methods. An alanine scan can be used to identify which amino acid residues in a protein can tolerate an amino acid substitution. In one example, the biological activity of the protein is not decreased by more than 25%, for example not more than 20%, for example not more than 10%, when an alanine, or other conservative amino acid (such as those listed below), is substituted for one or more native amino acids.

Examples of amino acids which can be substituted for an original amino acid in a protein and which are regarded as conservative substitutions include, but are not limited to: Ser for Ala; Lys for Arg; Gln or His for Asn; Glu for Asp; Ser for Cys; Asn for Gln; Asp for Glu; Pro for Gly; Asn or Gln for His; Leu or Val for Ile; Ile or Val for Leu; Arg or Gln for Lys; Leu or Ile for Met; Met, Leu or Tyr for Phe; Thr for Ser; Ser for Thr; Tyr for Trp; Trp or Phe for Tyr; and Ile or Leu for Val.

Further information about conservative substitutions can be found in, among other locations in, Ben-Bassat *et al.*, (*J. Bacteriol.* 169:751-7, 1987), O'Regan *et al.*, (*Gene* 77:237-51, 1989), Sahin-

Toth *et al.*, (*Protein Sci.* 3:240-7, 1994), Hochuli *et al.*, (*Bio/Technology* 6:1321-5, 1988) and in standard textbooks of genetics and molecular biology.

5 Ebola virus. A highly contagious hemorrhagic virus named after a river in the Democratic Republic of the Congo (formerly Zaire) in Africa, where it was first recognized. Ebola is one of two members of a family of RNA viruses called the Filoviridae. There are four identified subtypes of Ebola virus. Three of the four have caused disease in humans: Ebola-Zaire, Ebola-Sudan, and Ebola-Ivory Coast. The fourth, Ebola-Reston, has caused disease in nonhuman primates, but not in humans.

10 Ebola hemorrhagic fever (Ebola HF) is a severe, often fatal disease in humans and nonhuman primates (for example, monkeys, gorillas, and chimpanzees) that is caused by Ebola virus infection. Diagnosing Ebola HF in a recently infected individual can be difficult because early symptoms, such as red eyes and a skin rash, are nonspecific to the virus and are seen in other subjects with diseases that occur much more frequently. Antigen-capture enzyme-linked immunosorbent assay (ELISA) testing, IgM ELISA, PCR, and virus isolation can be used to diagnose a case of Ebola HF within a few days after the onset of symptoms. Subjects tested later in the course of the disease, 15 or after recovery, can be tested for IgM and IgG antibodies. The disease also can be diagnosed retrospectively in deceased patients by using immunohistochemistry testing, virus isolation, or PCR.

Encodes: Unless evident from its context, includes DNA sequences that encode a polypeptide, as the term is typically used, as well as DNA sequences that are transcribed into inhibitory antisense molecules.

20 **Expression:** With respect to a gene sequence, refers to transcription of the gene and, as appropriate, translation of the resulting mRNA transcript to a protein. Thus, expression of a protein coding sequence results from transcription and translation of the coding sequence.

Functional deletion: A mutation, partial or complete deletion, insertion, or other variation made to a gene sequence that inhibits production of the gene product or renders the gene product non- 25 functional. For example, a functional deletion of a Rab9 gene in a cell results in a cells having non-functional Rab9 protein, which results in the cell having an increase resistance to infection by a pathogen that uses a lipid raft.

Gene. A nucleic acid sequence that encodes a polypeptide under the control of a regulatory sequence, such as a promoter or operator. A gene includes an open reading frame encoding a polypeptide of the present disclosure, as well as exon and (optionally) intron sequences. An intron is 30 a DNA sequence present in a given gene that is not translated into protein and is generally found between exons. The coding sequence of the gene is the portion transcribed and translated into a polypeptide (*in vivo*, *in vitro* or *in situ*) when placed under the control of an appropriate regulatory sequence. The boundaries of the coding sequence can be determined by a start codon at the 5' (amino) terminus and a stop codon at the 3' (carboxyl) terminus. If the coding sequence is intended 35 to be expressed in a eukaryotic cell, a polyadenylation signal and transcription termination sequence can be included 3' to the coding sequence.

 Transcriptional and translational control sequences include, but are not limited to, DNA regulatory sequences such as promoters, enhancers, and terminators that provide for the expression of

the coding sequence, such as expression in a host cell. A polyadenylation signal is an exemplary eukaryotic control sequence. A promoter is a regulatory region capable of binding RNA polymerase and initiating transcription of a downstream (3' direction) coding sequence. Additionally, a gene can include a signal sequence at the beginning of the coding sequence of a protein to be secreted or
5 expressed on the surface of a cell. This sequence can encode a signal peptide, N-terminal to the mature polypeptide, which directs the host cell to translocate the polypeptide.

Host Cell. Any cell that can be infected with a virus or other pathogen, such as a bacterium. A host cell can be prokaryotic or eukaryotic, such as a cell from an insect, crustacean, mammal, bird, reptile, yeast, or a bacteria such as *E. coli*. Exemplary host cells include, but are not limited to,
10 mammalian B-lymphocyte cells. Examples of viruses include, but are not limited to HIV, influenza A, and Ebola.

The host cell can be part of an organism, or part of a cell culture, such as a culture of mammalian cells or a bacterial culture. A host nucleic acid is a nucleic acid present in a host cell that expresses a host protein. Decreasing or inhibiting the interaction between a host polypeptide or host
15 nucleic acid and a virus or viral protein can occur *in vitro*, *in vivo*, and *in situ* environments.

Human Immunodeficiency Virus (HIV). A retrovirus that causes immunosuppression in humans and leads to a disease complex known as acquired immunodeficiency syndrome (AIDS). This immunosuppression results from a progressive depletion and functional impairment of T lymphocytes expressing the CD4 cell surface glycoprotein. The loss of CD4 helper/inducer T cell
20 function may underlie the loss of cellular and humoral immunity leading to the opportunistic infections and malignancies seen in AIDS.

Depletion of CD4 T cells results from the ability of HIV to selectively infect, replicate in, and ultimately destroy these T cells (for example see Klatzmann *et al.*, *Science* 225:59, 1984). CD4 itself is an important component, and in some examples an essential component, of the cellular
25 receptor for HIV.

HIV subtypes can be identified by particular number, such as HIV-1 and HIV-2. In the HIV life cycle, the virus enters a host cell in at least three stages: receptor docking, viral-cell membrane fusion, and particle uptake (D'Souza *et al.*, *JAMA* 284:215, 2000). Receptor docking begins with a gp120 component of a virion spike binding to the CD4 receptor on the host cell. Conformational
30 changes in gp120 induced by gp120-CD4 interaction promote an interaction between gp120 and either CCR5 or CXCR4 cellular co-receptors. The gp41 protein then mediates fusion of the viral and target cell membranes. More detailed information about HIV can be found in Coffin *et al.*, *Retroviruses* (Cold Spring Harbor Laboratory Press, 1997).

Hybridization. Hybridization of a nucleic acid occurs when two complementary nucleic
35 acid molecules undergo an amount of hydrogen bonding to each other. The stringency of hybridization can vary according to the environmental conditions surrounding the nucleic acids, the nature of the hybridization method, and the composition and length of the nucleic acids used. For example, temperature and ionic strength (such as Na⁺ concentration) can affect the stringency of hybridization. Calculations regarding hybridization conditions required for attaining particular

degrees of stringency are discussed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001); and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes Part I*, Chapter 2 (Elsevier, New York, 1993).

5 The T_m is the temperature at which 50% of a given strand of nucleic acid is hybridized to its complementary strand. The T_m of a particular nucleic acid can be determined by various methods, such as observing the transition state between a single-stranded and double-stranded state during a temperature change, such as heating a dsDNA from about 30°C to about 100°C, and detecting when the dsDNA denatures to ssDNA. This can be accomplished by determining a melting profile for the
10 nucleic acid. For longer nucleic acid fragments, such as PCR products, the nearest-neighbor method can be used to determine T_m (Breslauer *et al.*, *Proc. Natl. Acad. Sci. USA* 83:3746-50, 1986). Additionally, MeltCalc software can be used to determine T_m (Schütz and von Ahsen, *Biotechniques* 30:8018-24, 1999).

For purposes of this disclosure, “stringent conditions” encompass conditions under which
15 hybridization only will occur if there is less than 25% mismatch between the hybridization molecule and the target sequence. “Moderate stringency” conditions are those under which molecules with more than 25% sequence mismatch will not hybridize; conditions of “medium stringency” are those under which molecules with more than 15% mismatch will not hybridize, and conditions of “high stringency” are those under which sequences with more than 10% mismatch will not hybridize.
20 Conditions of “very high stringency” are those under which sequences with more than 5% mismatch will not hybridize.

Moderately stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM KPO₄ (pH 7.4), 5X SSC, 5X Denhart’s solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate,
25 and 1-15 ng/mL probe (about 5x10⁷ cpm/µg), while the washes are performed at about 50°C with a wash solution containing 2X SSC and 0.1% sodium dodecyl sulfate.

Highly stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM KPO₄ (pH 7.4), 5X SSC, 5X Denhart’s solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate, and 1-15
30 ng/mL probe (about 5x10⁷ cpm/µg), while the washes are performed at about 65°C with a wash solution containing 0.2X SSC and 0.1% sodium dodecyl sulfate.

Infection. The entry, replication, insertion, lysis or other event or process involved with the pathogenesis of a virus or other infectious agent into a host cell. Thus, decreasing infection includes decreasing entry, replication, insertion, lysis, or other pathogenesis of a virus or other pathogen into a
35 cell or subject, or combinations thereof. Infection includes the introduction of an infectious agent, such as a non-recombinant virus, recombinant virus, plasmid, bacteria, prion, eukaryotic microbe, or other agent capable of infecting a host, such as the cell of a subject.

In another example, infection is the introduction of a recombinant vector into a host cell via transduction, transformation, transfection, or other method. Vectors include, but are not limited to,

viral, plasmid, cosmid, and artificial chromosome vectors. For example, a recombinant vector can include an antisense molecule, RNAi molecule, or siRNA that recognizes any target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants, fusions, or fragments thereof, as well as SEQ ID NOS: 1-227, 229, and 231 themselves.

5 **Influenza virus.** A virus that causes respiratory disease or influenza ("the flu") and can lead to a secondary infection in the host, such as a bacterial infection of the lungs. Three types of influenza are currently known: influenza A, influenza B, and influenza C. Influenza A is the most common form of the virus and is capable of infection humans and non-human animals, such as pigs, horses, chickens, ducks and other birds.

10 The viral genome includes eight RNA molecules. HA, which encodes hemagglutinin (three hemagglutinin subtypes: H1, H2, and H3); M, which encodes two matrix proteins based on two different open reading frames within the nucleic acid sequence; NA encodes for neuraminidase; NP encodes the nucleoprotein; NS encodes two non-structural proteins based on different open reading frames within the nucleic acid sequence; and three genes that encode RNA polymerases (PA, PB1, 15 PB2). The influenza virus can be categorized into subtypes on the bases of the surface glycoproteins.

The replication cycle of the influenza virus begins with binding of the viral hemagglutinin molecules to the surface carbohydrate of epithelial cell of a host cell, which draws the virus into the cell by receptor-mediated endocytosis. The viral membrane fuses with the endocytotic vesicle membrane, allowing the RNA molecules of the viral genome to enter the interior of the cell where 20 these molecules later enter the cell nucleus and are replicated into viral-complementary RNA and new viral RNA and transcribed into viral mRNA, which are transported into the cytosol where they are translated into the proteins of new viral particles. After viral particles are assembled into new viruses, the neuraminidase glycoproteins aid in the budding of the viruses from the cellular membrane of the host cell, thus releasing new viruses capable of infecting other host cells.

25 **Isolated:** An "isolated" biological component (such as a nucleic acid or protein) has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, such as other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids and proteins which have been "isolated" include nucleic acids and proteins purified by standard purification methods. The term 30 also embraces nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids, proteins and peptides.

35 **Nucleic acid.** A deoxyribonucleotide or ribonucleotide polymer in either single (ss) or double stranded (ds) form, and can include analogues of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally occurring nucleotides. In some examples, a nucleic acid is a nucleotide analog.

Unless otherwise specified, any reference to a nucleic acid molecule includes the reverse complement of nucleic acid. Except where single-strandedness is required by the text herein (for example, a ssRNA molecule), any nucleic acid written to depict only a single strand encompasses both strands of a corresponding double-stranded nucleic acid. For example, depiction of a plus-strand

of a dsDNA also encompasses the complementary minus-strand of that dsDNA. Additionally, reference to the nucleic acid molecule that encodes a specific protein, or a fragment thereof, encompasses both the sense strand and its reverse complement.

In particular examples, a nucleic acid includes a nucleotide sequence shown in any of SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof. In other examples, a nucleic acid has a nucleotide sequence including a target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof, such as the corresponding cDNA or mRNA of SEQ ID NOS: 1-227, 229, and 231.

The fragment can be any portion of the nucleic acid corresponding to at least 5 contiguous bases from any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229, and 231, for example at least 20 contiguous bases, at least 50 contiguous bases, at least 100 contiguous bases, at least 250 contiguous bases, or even at least 500 or more contiguous bases. A fragment can be chosen from a particular portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as a particular half, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, or smaller portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. Fragments of the nucleic acids described herein can be used as probes and primers.

Oligonucleotide. A linear polynucleotide (such as DNA or RNA) sequence of at least 9 nucleotides, for example at least 15, 18, 24, 25, 30, 50, 100, 200 or even 500 nucleotides long. In particular examples, an oligonucleotide is about 6-50 bases, for example about 10-25 bases, such as 12-20 bases.

An oligonucleotide analog refers to moieties that function similarly to oligonucleotides, but have non-naturally occurring portions. For example, oligonucleotide analogs can contain non-naturally occurring portions, such as altered sugar moieties or inter-sugar linkages, such as a phosphorothioate oligodeoxynucleotide. Functional analogs of naturally occurring polynucleotides can bind to RNA or DNA, and include peptide nucleic acid (PNA) molecules.

Open reading frame (ORF). A series of nucleotide triplets (codons) coding for amino acids without any internal termination codons. These sequences are usually translatable into a peptide.

Operably linked. A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

Pathogen: A disease-producing agent. Examples include, but are not limited to viruses, bacteria, and fungi.

Pharmaceutical agent or drug: A chemical compound or composition capable of inducing a desired therapeutic or prophylactic effect when administered to a subject, alone or in combination with another therapeutic agent(s) or pharmaceutically acceptable carriers. In a particular example, a

pharmaceutical agent decreases or even inhibits infection of a cell, such as the cell of a subject, by a pathogen, such as a virus.

Polymorphism. A polymorphism exists when two or more versions of a nucleic acid sequence exist within a population of subjects. For example, a polymorphic nucleic acid can be one where the most common allele has a frequency of 99% or less. Different alleles can be identified according to differences in nucleic acid sequences, and genetic variations occurring in more than 1% of a population (which is the commonly accepted frequency for defining polymorphism) are useful polymorphisms for certain applications.

The allelic frequency (the proportion of all allele nucleic acids within a population that are of a specified type) can be determined by directly counting or estimating the number and type of alleles within a population. Polymorphisms and methods of determining allelic frequencies are discussed in Hartl, D.L. and Clark, A.G., *Principles of Population Genetics*, Third Edition (Sinauer Associates, Inc., Sunderland Massachusetts, 1997), particularly in chapters 1 and 2.

Preventing or treating a disease: "Preventing" a disease refers to inhibiting the full development of a disease, for example preventing development of a viral infection. "Treatment" refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition related to a viral infection, such as inhibiting or decreasing viral infection.

Probes and primers. A probe includes an isolated nucleic acid attached to a detectable label or other reporter molecule. Typical labels include, but are not limited to radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed for example in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989) and Ausubel *et al.* (*In Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1998).

Primers are short nucleic acid molecules, such as DNA oligonucleotides ten nucleotides or more in length. Longer DNA oligonucleotides can be about 15, 20, 25, 30 or 50 nucleotides or more in length. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then the primer extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, for example by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods.

Nucleic acid probes and primers can be prepared based on the nucleic acid molecules of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, as indicators of resistance to infection. Probes and primers can be based on fragments or portions of these nucleic acid molecules, or on the reverse complement of these sequences, as well as probes and primers to 5' or 3' regions of the nucleic acids.

The specificity of a probe or primer increases with its length. Thus, for example, a primer that includes 30 consecutive nucleotides of a β -chimerin or Rab9 gene will anneal to a target sequence, such as another homolog of a β -chimerin or Rab9 gene, respectively, with a higher specificity than a

corresponding primer of only 15 nucleotides. Thus, to obtain greater specificity, probes and primers can be selected that include at least 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides of a nucleic acid disclosed herein.

Protein coding sequence or a sequence that encodes a peptide: A nucleic acid sequence
5 that is transcribed (in the case of DNA) and is translated (in the case of mRNA) into a peptide *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, cDNA from procaryotic or eukaryotic mRNA, genomic DNA sequences from procaryotic or eukaryotic DNA, and
10 even synthetic DNA sequences. A transcription termination sequence is usually be located 3' to the coding sequence.

Purified. The term purified does not require absolute purity; rather, it is a relative term. Thus, for example, a purified peptide preparation is one in which the peptide or protein is more enriched than the peptide or protein is in its environment within a cell, such that the peptide is
15 substantially separated from cellular components (nucleic acids, lipids, carbohydrates, and other polypeptides) that may accompany it. In another example, a purified peptide preparation is one in which the peptide is substantially-free from contaminants, such as those that might be present following chemical synthesis of the peptide.

In one example, an peptide is purified when at least 60% by weight of a sample is composed
20 of the peptide, for example when 75%, 95%, or 99% or more of a sample is composed of the peptide, such as a β -chimerin or Rab9 peptide. Examples of methods that can be used to purify proteins, include, but are not limited to the methods disclosed in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, Ch. 17). Protein purity can be determined by, for example, polyacrylamide gel electrophoresis of a protein sample, followed by visualization of
25 a single polypeptide band upon staining the polyacrylamide gel; high-pressure liquid chromatography; sequencing; or other conventional methods.

Rab9: The term Rab9 includes any Rab9 gene, cDNA, RNA, or protein from any organism and that is a Rab9 that can transport late endosomes to trans-golgi and function as a ras-like GTPase. In some examples, Rab9 is involved in lipid raft formation.

30 Examples of native Rab9 nucleic acid sequences include, but are not limited to, target sequences associated with SEQ ID NOS: 118 and 119. Examples of Rab9 amino acid sequences include, but are not limited to: Genbank Accession Nos: BC017265.2 and NM_004251.3 (cDNA) as well as P51151 and AAH17265 (proteins). In one example, a Rab9 sequence includes a full-length wild-type (or native) sequence, as well as Rab9 allelic variants, variants, fragments, homologs or
35 fusion sequences that retain the ability to transport late endosomes to trans-golgi. In certain examples, Rab9 has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native Rab9.

In other examples, Rab9 has a sequence that hybridizes to a sequence set forth in GenBank Accession No. BC017265.2 or NM_004251.3, and retains Rab9 activity.

Recombinant. A recombinant nucleic acid or protein is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination can be accomplished, for example, by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acids or proteins, for example, by genetic engineering techniques.

RNA interference (RNAi): A post-transcriptional gene silencing mechanism mediated by double-stranded RNA (dsRNA). Introduction of dsRNA into cells, such as RNAi compounds or siRNA compounds, induces targeted degradation of RNA molecules with homologous sequences. RNAi compounds are typically longer than an siRNA molecule. For example, an RNAi molecule can be at least about 25 nucleic acids, at least about 27 nucleic acids, or even at least about 400 nucleotides in length.

RNAi compounds can be used to modulate transcription, for example, by silencing genes, such as Rab9, β -chimerin, or combinations thereof. In certain examples, an RNAi molecule is directed against a certain target gene, such as Rab9, β -chimerin, or combinations thereof, and is used to decrease viral infection.

Sequence identity: The similarity between nucleic acid or amino acid sequences is expressed in terms of the similarity between the sequences. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or variants of a protein or nucleic acid disclosed herein, such as target sequences associated with SEQ ID NOS: 1-232, and their corresponding cDNA and protein sequences, will possess a relatively high degree of sequence identity when aligned using standard methods.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman and Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; Higgins and Sharp, *Gene* 73:237-44, 1988; Higgins and Sharp, *CABIOS* 5:151-3, 1989; Corpet *et al.*, *Nucl. Acids Res.* 16:10881-90, 1988; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; and Altschul *et al.*, *Nature Genet.* 6:119-29, 1994;

The NCBI Basic Local Alignment Search Tool (BLASTTM) (Altschul *et al.*, *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx.

Variants of a peptide, such as a peptide encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, as well as any target sequence associated with SEQ ID NOS: 228, 230, and 232, are typically characterized by possession of at least 70% sequence identity counted over the full length alignment with the amino acid sequence encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, or 231, using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence

cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment is performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 80%, at least 90%, at least 95%, at least 98%, or even at least 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs and variants will typically possess at least 80% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 98% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are described at the website that is maintained by the National Center for Biotechnology Information in Bethesda, Maryland. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided.

Similar methods can be used to determine the sequence identity between two or more nucleic acids. To compare two nucleic acid sequences, the BLASTN options can be set as follows: -i is set to a file containing the first nucleic acid sequence to be compared (such as C:\seq1.txt); -j is set to a file containing the second nucleic acid sequence to be compared (such as C:\seq2.txt); -p is set to blastn; -o is set to any desired file name (such as C:\output.txt); -q is set to -1; -r is set to 2; and all other options are left at their default setting. For example, the following command can be used to generate an output file containing a comparison between two sequences: C:\B12seq -i c:\seq1.txt -j c:\seq2.txt -p blastn -o c:\output.txt -q -1 -r 2.

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the sequence set forth in the identified sequence, or by an articulated length (for example, 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1154 nucleotides is 75.0 percent identical to the test sequence (for example, $1166 \div 1554 \times 100 = 75.0$). The percent sequence identity value is rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 20-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (for example, $15 \div 20 \times 100 = 75$).

| | | |
|----------------------|---------------------|----|
| | 1 | 20 |
| Target Sequence: | AGGTCGTGTACTGTCA | |
| | | |
| Identified Sequence: | ACGTGGTGAAGTCCAGTGA | |

The nucleic acids disclosed herein include nucleic acids have nucleotide sequences that are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% identical to the nucleotide sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. In particular examples, a nucleic acid is substantially similar to the nucleotide sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. A first nucleic acid is "substantially similar" to a second nucleic acid if, when the first nucleic acid is optimally aligned (with appropriate nucleotide deletions or gap insertions) with the second nucleic acid (or its complementary strand) and there is nucleotide sequence identity of at least about 90%, for example at least about 95%, at least 98% or at least 99% identity. An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid molecules that all encode substantially the same protein.

Short interfering or interrupting RNA (siRNA). Double-stranded RNAs that can induce sequence-specific post-transcriptional gene silencing, thereby decreasing or even inhibiting gene expression. In some examples, siRNA molecules are about 19-23 nucleotides in length, such as at least 21 nucleotides, for example at least 23 nucleotides.

In one example, siRNA triggers the specific degradation of homologous RNA molecules, such as mRNAs, within the region of sequence identity between both the siRNA and the target RNA. For example, WO 02/44321 discloses siRNAs capable of sequence-specific degradation of target mRNAs when base-paired with 3' overhanging ends. The direction of dsRNA processing determines whether a sense or an antisense target RNA can be cleaved by the produced siRNA endonuclease complex. Thus, siRNAs can be used to modulate transcription, for example, by silencing genes, such as Rab9, β -chimerin, or combinations thereof. The effects of siRNAs have been demonstrated in cells from a variety of organisms, including *Drosophila*, *C. elegans*, insects, frogs, plants, fungi, mice and humans (for example, WO 02/44321; Gitlin *et al.*, *Nature* 418:430-4, 2002; Caplen *et al.*, *Proc. Natl. Acad. Sci.* 98:9742-9747, 2001; and Elbashir *et al.*, *Nature* 411:494-8, 2001).

In certain examples, siRNAs are directed against certain target genes, such as Rab9, β -chimerin, or combinations thereof, to confirm results of the gene-trap method used against the same nucleic acid sequence.

Specific binding agent. An agent that binds substantially only to a defined target. For example, a protein-specific binding agent binds substantially only the specified protein and a nucleic acid specific binding agent binds substantially only the specified nucleic acid.

As used herein, the term "protein [X] specific binding agent" includes anti-[X] protein antibodies (including polyclonal or monoclonal antibodies and functional fragments thereof) and other agents (such as soluble receptors) that bind substantially only to the [X] protein. In this context, [X] refers to any specific or designated protein, for instance β -chimerin, Rab9, or any protein listed in Table

1 or encoded by a target sequence associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof).

Anti-[X] protein antibodies can be produced using standard procedures such as those described in Harlow and Lane (*Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press: 5 Cold Spring Harbor, 1998). Antibodies can be polyclonal or monoclonal antibodies, humanized antibodies, Fab fragments, F(ab')₂ fragments, single chain antibodies, or chimeric antibodies. For example, polyclonal antibodies can be produced by immunizing a host animal by injection with polypeptides described herein, including the target sequences associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof). The production of monoclonal antibodies can be 10 accomplished by a variety of methods, such as the hybridoma technique (Kohler and Milstein, *Nature* 256:495-7, 1975), the human B-cell technique (Kosbor *et al.*, *Immunology Today* 4:72, 1983), or the EBV-hybridoma technique (Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, 1983). Additionally, chimeric antibodies can be produced (for example, see Morrison *et al.*, *J. Bacteriol.* 159:870, 1984; Neuberger *et al.*, *Nature* 312:604-8, 1984; and Takeda *et al.*, *Nature* 15 314:452-4, 1985), as well as single-chain antibodies (for example, see U.S. Pat. Nos. 5,476,786; 5,132,405; and 4,946,778).

The determination that a particular agent binds substantially only to the specified protein readily can be made by using or adapting routine procedures. For example, Western blotting can be used to determine that a given protein binding agent, such as an anti-[X] protein monoclonal antibody, 20 binds substantially only to the [X] protein. Other assays include, but are not limited to, competitive and non-competitive homogenous and heterogeneous enzyme-linked immunosorbent assays (ELISA) as symmetrical or asymmetrical direct or indirect detection formats; "sandwich" immunoassays; immunodiffusion assays; in situ immunoassays (for example, using colloidal gold, enzyme or radioisotope labels); agglutination assays; complement fixing assays; immunoelectrophoretic assays; 25 enzyme-linked immunospot assays (ELISPOT); radioallergosorbent tests (RAST); fluorescent tests, such as used in fluorescent microscopy and flow cytometry; Western, grid, dot or tissue blots; dip-stick assays; halogen assays; or antibody arrays (for example, see O'Meara and Tovey, *Clin. Rev. Allergy Immunol.*, 18:341-95, 2000; Sambrook *et al.*, 2001, Appendix 9; Simonnet and Guilloteau, in: *Methods of Immunological Analysis*, Masseyeff *et al.* (Eds.), VCH, New York, 1993, pp. 270-388).

30 A specific binding agent also can be labeled for direct detection (see Chapter 9, Harlow and Lane, *Antibodies: A Laboratory Manual*, 1988). Suitable labels include (but are not limited to) enzymes (such as alkaline phosphatase (AP) or horseradish peroxidase (HRP)), fluorescent labels, colorimetric labels, radioisotopes, chelating agents, dyes, colloidal gold, ligands (such as biotin), and chemiluminescent agents.

35 Shorter fragments of antibodies can also serve as specific binding agents. For instance, Fabs, Fvs, and single-chain Fvs (SCFvs) that bind to a specified protein would be specific binding agents. These antibody fragments include: (1) Fab, the fragment containing a monovalent antigen-binding fragment of an antibody molecule produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an

antibody molecule obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) (Fab')₂, the fragment of the antibody obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; (4) F(ab')₂, a dimer of two Fab' fragments held together by two disulfide bonds; (5) Fv, a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (6) single chain antibody ("SCA"), a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Methods of making these fragments are routine. For example, construction of Fab expression libraries permits the rapid and easy identification of monoclonal Fab fragments with the desired specificity for a protein described herein.

Subject: Living multi-cellular vertebrate organisms, including human and veterinary subjects, such as cows, pigs, horses, dogs, cats, birds, reptiles, and fish.

Target sequences associated with SEQ ID NO: When used herein, this phrase refers to any nucleic acid sequence, amino acid sequence, or combination of nucleic acid and amino acid sequences, that are involved in viral infection, and therefore serve as targets for inhibiting viral infection, and which are or include a specified SEQ ID NO, are involved in the expression of the SEQ ID NO, or are peptide (including protein) sequences that are expressed by such specified SEQ ID NO. Although a target sequence may refer to a SEQ ID NO of a sequence obtained from a particular species, the target sequences also include homologues of the sequence from other related species, such as other mammals. For example, the phrase "target sequences associated with SEQ ID NO. X" can refer to the entire gene sequence of which the particular SEQ ID NO X is a part, the appropriate coding sequence, a promoter sequence associated with the gene, or the corresponding protein sequence, as well as variants, fragments, homologues, and fusions thereof that retain the activity of the native sequence.

For example, when using the phrase "sequences associated with SEQ ID NOS: 21-22," this term encompasses β -chimerin genomic sequences, endogenous promoter sequences that promote the expression of β -chimerin, coding sequences, and β -chimerin proteins, as well as variants, fragments homologues and fusions thereof that retain the activity of the native sequence. A particular cDNA sequence associated with SEQ ID NOS: 21-22 is provided in GenBank Accession No. NM_004067, and a particular protein sequence associated with SEQ ID NOS: 21-22 is provided in NP_004058.1.

The term "a GenBank Accession No. associated with SEQ ID NO. X" refers to a GenBank Accession No. that includes SEQ ID NO. X, or is a homolog of SEQ ID NO: X from another mammal, for example a human homolog. The GenBank Accession No. may, in some examples, also identify a coding sequence of an open reading frame, and the sequence of the protein encoded by SEQ ID NO. X.

Although sequences are provided herein that encode (or are included within sequences that encode) host proteins that are involved in viral infection, it should be understood that the ultimate goal is to interfere with the activity of the protein that has been identified to be involved in viral

pathogenesis. Such interference can be at either the level of the nucleic acid that encodes the protein (for example by reducing or otherwise disrupting expression of the protein), or at the level of the protein itself (for example by interfering with the activity of the protein, or its interaction with the virus). The disclosure of specific techniques for achieving these goals in particular species should not
5 be interpreted to limit the method to these particular techniques, or to particular species in which the viral interaction is first identified. The identification of the viral interaction in one species indicates the importance of the interaction between the virus and the protein in that species, as well as the interaction of the virus with homologues of that protein in other species.

Target sequence of a nucleic acid: A portion of a nucleic acid that, upon hybridization to a
10 therapeutically effective oligonucleotide or oligonucleotide analog, results in reduction or even inhibition of infection by an infectious agent. An antisense or a sense molecule can be used to target a portion of dsDNA, since either can interfere with the expression of that portion of the dsDNA. The antisense molecule can bind to the plus strand, and the sense molecule can bind to the minus strand. Thus, target sequences can be ssDNA, dsDNA, and RNA.

Therapeutically active molecule: An agent, such as a protein, antibody or nucleic acid,
15 that can decrease expression of a host protein involved in viral infection (such as those listed in Table 1 or target sequences associated with any of SEQ ID NOS: 1-232, or can decrease an interaction between a host protein involved in viral infection and a viral protein, such as HIV, Ebola, or influenza A, as measured by clinical response (for example, a decrease in infection by a virus, such as an
20 inhibition of infection). Therapeutically active agents also include organic or other chemical compounds that mimic the effects of the therapeutically effective peptide or nucleic acids.

Therapeutically Effective Amount: An amount of a pharmaceutical preparation that alone, or together with an additional therapeutic agent(s), induces the desired response. The preparations disclosed herein are administered in therapeutically effective amounts.

In one example, a desired response is to decrease or inhibit viral infection of a cell, such as a
25 cell of a subject. Viral infection does not need to be completely inhibited for the pharmaceutical preparation to be effective. For example, a pharmaceutical preparation can decrease viral infection by a desired amount, for example by at least 20%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or even at least 100%, as compared to an amount of
30 viral infection in the absence of the pharmaceutical preparation. This decrease or inhibition can result in halting or slowing the progression of, or inducing a regression of a pathological condition caused by the viral infection, or which is capable of relieving signs or symptoms caused by the condition.

In another or additional example, it is an amount sufficient to partially or completely
35 alleviate symptoms of viral infection within a host subject. Treatment can involve only slowing the progression of the infection temporarily, but can also include halting or reversing the progression of the infection permanently.

Effective amounts of the therapeutic agents described herein can be determined in many different ways, such as assaying for a reduction in the rate of infection of cells or subjects, a reduction in the viral load within a host, improvement of physiological condition of an infected subject, or

increased resistance to infection following exposure to the virus. Effective amounts also can be determined through various *in vitro*, *in vivo* or *in situ* assays, including the assays described herein.

The disclosed therapeutic agents can be administered in a single dose, or in several doses, for example daily, during a course of treatment. However, the effective amount of can be dependent
5 on the source applied (for example a nucleic acid isolated from a cellular extract versus a chemically synthesized and purified nucleic acid), the subject being treated, the severity and type of the condition being treated, and the manner of administration. In addition, the disclosed therapeutic agents can be administered alone, or in the presence of a pharmaceutically acceptable carrier, or in the presence of other therapeutic agents, for example other anti-viral agents.

10 **Transduced and Transformed:** A virus or vector "transduces" or "transfects" a cell when it transfers nucleic acid into the cell. A cell is "transformed" by a nucleic acid transduced into the cell when the DNA becomes stably replicated by the cell, either by incorporation of the nucleic acid into the cellular genome, or by episomal replication. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell,
15 including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transfected: A transfected cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. The term transfection encompasses all techniques by which a nucleic acid molecule can be introduced into such a cell, including transfection with viral
20 vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transgene: An exogenous nucleic acid sequence supplied by a vector. In one example, a transgene includes any target sequence associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof), for example a nucleic acid that encodes a beta-chimerin or Rab9.

25 **Variants, fragments or fusions:** The disclosed nucleic acid sequences, such as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby, include variants, fragments, and fusions thereof that retain the native biological activity (such as playing a role in viral infection). DNA sequences which encode for a protein or fusion thereof, or a fragment or variant of thereof can be engineered to allow the protein to be expressed in eukaryotic
30 cells or organisms, bacteria, insects, and/or plants. To obtain expression, the DNA sequence can be altered and operably linked to other regulatory sequences. The final product, which contains the regulatory sequences and the therapeutic protein, is referred to as a vector. This vector can be introduced into eukaryotic, bacteria, insect, and/or plant cells. Once inside the cell the vector allows the protein to be produced.

35 **One of ordinary skill in the art will appreciate that the DNA can be altered in numerous ways without affecting the biological activity of the encoded protein. For example, PCR can be used to produce variations in the DNA sequence which encodes a protein. Such variants can be variants optimized for codon preference in a host cell used to express the protein, or other sequence changes that facilitate expression.**

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector can include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication, and can also include one or more selectable marker genes and other genetic elements. An insertional vector is capable of inserting itself into a host nucleic acid.

5 For example, recombinant lambda-phage vectors of host genomes (Coffin *et al.*, *Retroviruses*, Chapter 5).

Wild-type. A naturally occurring, non-mutated version of a nucleic acid sequence. Among multiple alleles, the allele with the greatest frequency within the population is usually (but not necessarily) the wild-type. The term "native" can be used as a synonym for "wild-type."

10

Nucleic Acids and Proteins Involved in Viral Infection

Examples of host nucleic acids and proteins that play a role in viral infection have been identified and are summarized in Table 1. These nucleic acids and proteins offer new targets for therapies that reduce or even inhibit or prevent viral infection, and offer new strategies for assessing the risk of infection among certain populations. While the target genes were identified in an assay

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using the recited virus, it is appreciated that infections agents such as viruses will share common pathways. Thus, the host sequences set forth below can be interfered with to decrease infection in a host cell.

Examples of viruses that can be inhibited are described in Virology, Volumes 1 and 2 by Bernard Fields, Second Edition, 1990, Raven Press. Exemplary viruses include, but are not limited to members of the family: Picornaviridae (such as Poliovirus, Coxsackievirus, Echovirus, Rhinovirus, and Hepatitis A and E); Calciviridae (such as Norwalk and related viruses); Togaviridae and Flaviviridae (such as hepatitis C, Alphavirus, and Rubella); Coronaviridae (such as SARS); Rhabdoviridae (such as Rabies); Filoviridae (such as Marburg and Ebola); Paramyxoviridae (such as Parainfluenza, Mumps, Measles, Hydra and Respiratory Syncytial virus); Orthomyxoviridae;

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Table 1: Examples of Host Genes and Proteins Implicated in Pathogenesis

| Nucleic Acid or Protein | Associated Virus | SEQ ID NO: | GenBank Accession Nos for cDNA and Protein |
|------------------------------|------------------|------------|--|
| T-cell receptor V beta chain | HIV | 1-19 | |

| | | | |
|---|------------------------|-------|---------------------------|
| T-cell receptor V-D-J beta 2.1 chain | HIV | 20 | |
| β -chimerin (CHN2) | HIV | 21-22 | NM_004067; NP_004058.1 |
| Malic enzyme 1 (ME1) | HIV and Influenza A | 23 | BC025246; AAH25246.1 |
| Hypothetical protein XP_174419 | HIV and Influenza A | 24 | |
| sequence from Chromosome 4q31.3-32 | HIV and Influenza A | 25-27 | |
| alpha satellite DNA | HIV | 28 | |
| LOC253788 and LOC219938; coagulation factor III (F3) and LOC91759 | HIV | 29 | |
| similar to KOX4 (LOC131880) and LOC166140 | HIV | 30 | |
| LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta | HIV | 31 | |
| ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC) | HIV | 32 | |
| KIAA0564 | HIV | 33 | |
| alpha satellite DNA; M96 protein | HIV | 34 | |
| hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2) | HIV | 35 | |
| | | | |
| Canis familiaris T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase (AMT) gene, dystroglycan (DAG1) gene, and bassoon (BSN) gene | Influenza A | 36-37 | |
| LIM domain containing preferred translocation partner in lipoma (LPP) | Influenza A | 38-48 | |
| sequence between LOC253121 and hyaluronan synthase 2 (HAS2) | Influenza A | 49 | |
| Testin 2 and Testin 3 (TES) | Influenza A | 50-57 | |
| PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 | Influenza A | 58-59 | |
| sequence between LOC149360 and LOC253961 | Influenza A | 60 | |
| sequence between KIAA1560 and Tectorin beta (TECTB) | Influenza A | 61 | |
| Cadherin related 23 (CDH23) | Influenza A | 62 | BC032581; AAH32581.1 - |
| Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10) | Influenza A | 63 | |
| | | | |

| | | | |
|--|-------|---------|----------------------------|
| exportin 5 (XPO5) and DNA polymerase eta (POLH) | Ebola | 64-66 | |
| heterogenous nuclear riboprotein C (C1/C2) (HNRPC) | Ebola | 67-75 | |
| alpha-endosulfine pseudogene (ENSAP) and LOC128741 | Ebola | 76 | |
| LOC222888 | Ebola | 77 | |
| LOC138421 and zinc finger protein 297B (ZNF297B) | Ebola | 78 | |
| sideroflexin 5 (SFXN5) | Ebola | 79 | AY044437; AAK95826 |
| importin 9 (FLJ10402) | Ebola | 80 | |
| T-cell receptor beta | Ebola | 81-82 | |
| similar to murine putative transcription factor ZNF131 (LOC135952) | Ebola | 83-99 | |
| KIAA1259 | Ebola | 100-101 | AB033085; NP_115572 |
| MURR1 and CCT4 | Ebola | 102 | |
| FLJ40773 and similar to ribosomal protein L24-like (LOC149360) | Ebola | 103 | |
| Testin 2 and 3 (TES) | Ebola | 104-107 | See above |
| polybromo 1 (PB1) | Ebola | 108 | NM_018165.2; NP_060635 |
| DNA damage inducible transcript 3 (DDIT3) and KIAA1887 | Ebola | 109 | |
| PDZ and LIM domain 1 (elfin) (PDLIM1) | Ebola | 110 | |
| LOC284803 | Ebola | 111-112 | |
| PRO0097 and FLJ31958 | Ebola | 113 | |
| small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1) | Ebola | 114-116 | |
| E3 ubiquitin ligase (SMURF2) and MGC40489 | Ebola | 117-119 | |
| Ras oncogene family member Rab9 | Ebola | 118-119 | |
| PRO1617 and retinoblastoma binding protein 1 (RBBP1) | Ebola | 120-122 | NM_000321; NP_000312.1 |
| region of chromosome 2q12 | Ebola | 123 | |
| elongation factor for selenoprotein translation | Ebola | 124 | NM_021937.1 NP_068756.1 |
| Transcription factor SMIF (HSA275986) | Ebola | 125-137 | |
| KIAA1026 | Ebola | 138 | |
| trinucleotide repeat containing 5 (TNRC5) | Ebola | 139 | |
| homogentisate 1,2-dioxygenase (HGD) | Ebola | 140 | |
| region of chromosome Xq23-24 | Ebola | 141 | |
| region of chromosome 4p15.3 | Ebola | 142 | |
| similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883) | Ebola | 143 | |

| | | | |
|---|-------|---------|-----------------------------|
| region of chromosome 2q21 | Ebola | 144 | |
| region of chromosome Xp11.4, including UPS9X | Ebola | 145 | |
| LOC221829 | Ebola | 146 | |
| U3 small nuclear RNA | Ebola | 147-154 | |
| integrin, beta 1 (ITGB1) | Ebola | 155-158 | BC020057; AAH20057.1 |
| acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1) | Ebola | 159 | |
| prospero-related homeobox 1 (PROX1) | Ebola | 160 | |
| FLJ20627 and FLJ12910 | Ebola | 161-173 | |
| PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7) | Ebola | 174 | |
| LOC131920 | Ebola | 175 | |
| region of chromosome 13q14 | Ebola | 176 | |
| neurotrophic tyrosine kinase, receptor, type 3 (NTRK3) | Ebola | 177 | |
| TERA protein and FLJ13224 | Ebola | 178-179 | |
| LOC284260 | Ebola | 180 | |
| POM (POM121 homolog) and ZP3 fusion (POMZP3) | Ebola | 181-182 | |
| DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064) | Ebola | 183 | |
| LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7) | Ebola | 184-186 | |
| Mus musculus 5S rRNA pseudogene (Rn5s-ps1) | Ebola | 187 | |
| ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2) | Ebola | 188-192 | |
| Down's syndrome cell adhesion molecule like 1 (DSCAML1) | Ebola | 193 | |
| LOC148529 | Ebola | 194 | |
| Huntingtin-associated protein interacting protein (HAPIP) | Ebola | 195 | NM_005338.4; NP_005329.3 |
| LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366) | Ebola | 196-200 | |
| hypothetical protein FLJ12910 | Ebola | 201-204 | |
| LOC350411 | Ebola | 205 | |
| allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2) | Ebola | 206 | |
| C10orf7 | Ebola | 207 | |
| LOC346658 and LOC340349 | Ebola | 208-209 | |
| region of chromosome 12q21 | Ebola | 210 | |
| LOC339248 and FLJ22659 | Ebola | 211 | |
| SR rich protein DKFZp564B0769 and | Ebola | 212 | |

| | | | |
|--|-------|---------|-----------------------------|
| hypothetical protein MGC14793 | | | |
| FLJ10439 | Ebola | 213-214 | NM_018093.1; NP_060563.1 |
| cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A | Ebola | 215-218 | |
| ribosomal protein S16 (RPS16) | Ebola | 219-220 | BC004324.2; AAH04324.1 |
| hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY) | Ebola | 221-222 | |
| calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK) | Ebola | 223-224 | |
| cyclin M2 (CNNM2) | Ebola | 225 | NM_017649.2; NP_060119.2 |
| AXL receptor tyrosine kinase (AXL) | Ebola | 226 | BC032229; AAH32229.1 |
| <i>Homo sapiens</i> chromosome 10 open reading frame 3 | Ebola | 227-228 | |
| <i>Homo sapiens</i> chromosome 10 open reading frame 3 (C10orf3) | Ebola | 229-230 | |
| <i>Homo sapiens</i> fer-1-like 3, myoferlin (<i>C. elegans</i>) | Ebola | 231-232 | NM_013451; NP_038479.1 |

Some of the host nucleic acids described in Table 1 and target sequences associated with SEQ ID NOS: 1-227, 229, and 231 encode polypeptides that are receptors or ligands recognized by a particular virus, such as HIV, influenza A, or the Ebola virus. For example, the T-cell receptor V beta and V-D-J beta 2.1 chain polypeptides are part of the T-cell receptor complex that are recognized by certain glycoproteins in the HIV envelope. Other host nucleic acids encode polypeptides that provide an enzymatic function related to a viral life cycle, such as the signaling pathways controlling viral packaging or enzymes involved in viral replications. For example, the β -chimerin rho-GTPase may mediate a cellular signal that initiates or triggers a process leading to passage of an HIV viral particle into the host cell. The data presented herein indicate that Rab9 is involved in pathogen infectivity, for example by interfering with trafficking of proteins and lipids within cells. In particular examples, it is demonstrated that Rab9 is involved in lipid raft formation, and that decreasing functional Rab9 and lipid rafts decreases the ability of pathogens, such as viruses and bacteria, that hijack lipid rafts to bud or be infectious.

Still other host nucleic acids participate in the life cycle of a virus. For example, a certain nucleotide sequence of a host nucleic acid, such as a gene within the host genome can be recognized during insertion and integration of a viral genome (reverse transcribed into DNA from the viral RNA genomic template) into the host genome. Viral integration is described in, for example, Coffin *et al.*, *Retroviruses*, Chapter 5.

The nucleic acids and proteins disclosed herein can be identified, isolated, and characterized using any number of techniques of molecular biology, including the specific methods and protocols described herein, such as in the examples below. In some examples, the nucleic acids were identified

and isolated using the Lexicon Genetics, Inc. (The Woodlands, TX) "gene trap" technology disclosed in U.S. Pat. Nos: 6,080,576; 6,136,566; 6,207,371; 6,139,833; 6,218,123 and 6,448,000.

Gene trap technology is a powerful method for cloning and identifying functional genes, as it marks a gene with a tag and simultaneously generates a corresponding genetic variation for that particular locus. The method involves introducing into a cell a DNA construct that can monitor and potentially disrupt the transcriptional activity of the region of the cell's genome into which it is inserted. The gene-trap method used to identify the host sequences is disclosed in U.S. Patent No. 6,448,000 (herein incorporated by reference).

Briefly, the gene trap protocol involves infecting a host cell (for example, a cell of a Sup T-1 cell line (human), MDCK cells (canine), or Vero cells (monkey)) with a recombinant vector (for example, U3neoSV1, FIG. 1). The recombinant vector includes a selectable marker or other sequence capable of being used to select infected host cells. However, the selectable marker or other sequence does not have a promoter at its 5' end. An exemplary selectable marker is a nucleic acid encoding resistance to an antibiotic (such as neomycin). A summary of the gene trap method is provided in FIGS. 2 and 3. Infection of the host cell is performed in culture under conditions that yield about one copy of the vector per cell. The vector incorporates into the host cell genome adjacent to an active promoter and interrupts or disrupts the transcription of a nucleic acid in the host cell (FIG. 2). The host promoter drives expression of the selectable marker or other sequence on the vector, and infected cells can then be selected. For example, if the vector carries a nucleic acid encoding neomycin resistance, cells can be selected on a medium that contains neomycin or G418, the neomycin analog for mammalian cells, depending on the type of host cell used.

The selected host cells are expanded in culture to form a library of cells that contain randomly disrupted host genes (FIG. 3). An aliquot of the library of cells is exposed to the appropriate virus, such as HIV, influenza A, or Ebola, to determine the effect of the disrupted host sequence on viral infection of the host cells. Host cells that survive the viral infection, or are relatively resistant to such infection (such as those cells that survive for a longer period of time than about at least 50% of the infected cells), can include one or more disrupted genes involved in viral infection. Thus, by using the vector one can decrease viral or pathogenic infection of a host cell or in a subject. Therefore, by identifying these disrupted genes that decreased or otherwise interfered with viral infection of the host cell, candidate sequences are identified that can be used as targets to decrease or inhibit viral infection.

Those host cells that survive viral infection, or are relatively resistant to such infection, are cloned, for example, by limit dilution using a chambered plate or by growth on methylcellulose. The interrupted host nucleic acid is identified using standard molecular biology methods. For example, host DNA can be isolated from the cell and digested using an appropriate restriction enzyme to free the 5' and 3' sequences adjacent the incorporated vector. The isolated DNA fragment can then be amplified, for example using PCR or by introducing the DNA fragment into a bacterial host cell then growing the bacteria. Once isolated, the host nucleic acid can be further characterized and analyzed.

For example, the nucleic acid can be sequenced and compared to other similar nucleic acids. Methods of using these nucleic acids, and the proteins encoded thereby, are discussed below.

Using these gene trap methods, several host molecules were identified that were previously not known to be involved in viral pathogenesis (SEQ ID NOS: 1-232, Table 1, and target sequences associated with SEQ ID NOS: 1-232). For example, the AMT gene (target sequences associated with SEQ ID NOS: 36 and 37) participates in influenza A infection of host cells. Fragments of host sequences involved in viral infection and pathogenesis can now be identified, even including fragments or sequences that were previously known to be important in the pathogenesis of intracellular pathogens. For example, although the T-cell receptor was previously implicated in HIV infection, the results disclosed herein demonstrate that the T-cell receptor V-D-J beta 2.1 chain (target sequences associated with SEQ ID NO: 20) is involved and in some examples required for HIV infection, and host cells lacking the T-cell receptor V-D-J beta 2.1 chain are unexpectedly highly resistant to HIV infection. Hence the V-D-J beta 2.1 chain is a target for anti-viral therapy at the DNA or polypeptide level, and other pathogenically active subcomponents of other known pathogenic sequences can also be identified with this method.

Examples of these host nucleic acid molecules are target sequences associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof) and summarized in Table 1. In addition to these specifically disclosed nucleotide sequences, a host nucleic acid can include nucleotide sequences that are similar to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as having at least 70% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 95% identity, at least 98% identity, or even at least 99% identity to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. The disclosed host nucleic acid sequences, and methods of using them, may comprise, consist, or consist essentially of any of the disclosed nucleic acid sequences shown in SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants or fragments thereof, or sequences that hybridize to the identified sequences under stringent or moderately stringent conditions.

The host nucleic acid molecules also include a fragment of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, such as a probe or primer as described below.

Host polypeptides corresponding to these nucleic acids also can be used to practice the disclosed methods. In some examples, the polypeptide includes an amino acid sequence that corresponds to a coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. However, host polypeptides can also include those having similar amino acid sequences, such as polypeptides that are at least 70% identical, at least 80% identical, at least 90% identical, at least 95% identical, at least 98% identical, or at least 99% identical to the amino acid sequences corresponding to translations of the coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. For example, the disclosed host polypeptides and methods of using them, may comprise, consist, or consist

essentially of an amino acid sequence corresponding to a translation of the nucleotide sequence in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, a target protein sequence associated with SEQ ID NOS: 228, 230, and 232, or any of the protein sequences listed in Table 1. Alternatively, the polypeptides include homologous polypeptides from other mammals (for example human, monkeys, and dogs).

The host polypeptide can have an amino acid sequence that varies by one or more conservative substitutions from the amino acid sequences of the proteins encoded by target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or from the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. In one example, there is no more than 1, 2, 3, 4, 5, or 10 conservative amino acid substitutions. In another example, there are 1, 2, 3, 4, 5 or 10 conservative amino acid substitutions. The effects of these amino acid substitutions, deletions, or additions on host polypeptides can be assayed, for example, by analyzing the ability of cells transformed with the derivative proteins to resist infection by the corresponding virus.

Also included are fragments of any host polypeptide encoded by any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, as well as fragments of the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. For example, a protein can include at least 5-500 contiguous amino acids of the protein, such as at least 6-200, at least 6-100, at least 10-100, at least 10-50, or at least 20-50 contiguous amino acids of the protein. A host polypeptide fragment can be at least 5, at least 10, at least 15, at least 25, at least 50, at least 100, at least 200, at least 500, or more amino acids of a polypeptide having an amino acid sequence corresponding to a coding region of the nucleotide sequence in any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant thereof, as well as target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232.

Fragments of a nucleic acid target sequences associated with SEQ ID NOS: 1-227, 229, and 231 can include 10-5000 contiguous nucleic acids, such as 12-1000, 12-500, 15-100, or 18-50 contiguous nucleic acids. A host nucleic acid fragment can be at least at least 5, at least 10, at least 15, at least 20, at least 25, at least 50, at least 100, at least 200, at least 500, at least 1000, at least 2000, at least 5000 or more contiguous nucleic acids in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant or fusion thereof.

Also included are host nucleic acids that encode the same polypeptide encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant of the polypeptide, or a fragment thereof. For example, a host nucleic acid provided by target sequences associated with SEQ ID NOS: 36-37 encodes AMT. A second host nucleic acid also can encode an AMT having the same amino acid sequence as the AMT encoded by target sequences associated with SEQ ID NOS: 36-37, a conservative variant of this AMT, or a fragment thereof, yet this second host nucleic acid can have a different nucleotide sequence than a target sequence associated with SEQ ID NOS: 36-37 due to the degeneracy of the genetic code.

Methods of Using Host Sequences to Decrease Viral Infection

The interaction between a host nucleic acid or polypeptide (such as target sequences associated with SEQ ID NOS: 1-232 and those shown in Table 1) and a virus or viral protein can be decreased or inhibited using the methods provided. Decreasing or inhibiting this interaction can be used to decrease viral infection of a host cell, and/or to decrease symptoms associated with a viral infection in a subject. For example, decreasing or even inhibiting the interaction of a host nucleic acid or polypeptide and a virus can decrease, inhibit, or even prevent infection of a host cell by that virus, or otherwise inhibit the progression or clinical manifestation of the viral infection. In addition, decreasing the interaction of a host nucleic acid or polypeptide and a virus can reduce or alleviate one or more symptoms associated with viral infection, such as a fever.

Several methods can be used to decrease or inhibit the interaction between a viral protein and a host protein or nucleic acid. The viral and host proteins or nucleic acids can be part of an *in vitro* solution, an *in vivo* expression system, or *in situ* with a host tissue or subject. The viral protein can be part of a larger molecule or complex, such as an envelope protein on the envelope of a mature virus or a fragment of a viral envelope. The host protein also can be part of a larger molecule or complex, such as a host polypeptide expressed as part of a fusion protein or contained as one subunit of a larger protein, such as a transport protein, cell receptor, structural protein, or an enzyme. A host nucleic acid can be part of a larger molecule, complex, organism or microorganism such as a host nucleic acid contained within its host genome, a recombinant vector, or a transgenic organism or microorganism (including both extrachromosomal molecules or genomic insertions).

In accordance with the disclosed methods, interaction is decreased or inhibited between a virus or viral protein and more than one (such as 2 or more, such as 3 or more) host nucleic acids or polypeptides. Decreasing or inhibiting the interactions of one or more host nucleic acids or polypeptides with one or more viral proteins can have additive or exponentially increasing effects. For example, it is believed that decreasing the interaction between a host T-cell receptor V-D-J beta 2.1 chain and HIV, or decreasing the activity of a host β -chimerin, within a host cell can enhance the inhibitory effect on HIV infection of that host cell compared to inhibiting the interaction of only one of the host polypeptides. Hence, the methods include interfering with an interaction between the virus or viral protein and more than one of the proteins associated with infection by the same virus.

For example, for infection with HIV, the method could interfere with one, or two or more (such as three or more) of the following: T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β -chimerin (CHN2); malic enzyme 1; Hypothetical protein XP_174419; sequence from Chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (such as RAP-2A; LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like).

For Ebola virus, examples of targets include one, or two or more (such as three or more) of the following: exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9; T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773 and similar to ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3 (DDIT3); KIAA1887; PDZ and LIM domain 1 (elfin) (PDLIM1); LOC284803; PRO0097 and FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2) and MGC40489; Rab9; PRO1617 and retinoblastoma binding protein 1 (RBBP1); region of chromosome 2q12; elongation factor for selenoprotein translation; transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5; homogentisate 1,2-dioxygenase; region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1; acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein; FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); 5S rRNA pseudogene; ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1; LOC148529; Huntingtin-associated protein interacting protein; LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1); HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658; LOC340349; region of chromosome 12q21; LOC339248; FLJ22659; SR rich protein DKFZp564B0769; hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1; sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16; hypothetical protein DKFZp434H0115; ATP citrate lyase; calnexin; protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2; AXL receptor tyrosine kinase; *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566); *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3); and *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*) (FER1L3), transcript variant 1.

For influenza, examples of targets include one, or two or more (such as three or more) of the following: T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase; dystroglycan; BSN; LIM domain containing preferred translocation partner in lipoma (LPP); sequence between LOC253121 and hyaluronan synthase 2 (HAS2); testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961;

sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; malic enzyme 1; hypothetical protein XP_174419; and sequence from chromosome 4q31.3-32.

In examples where a host polypeptide is a cell receptor or part of a cell receptor, decreasing
5 or preventing expression of the polypeptide, or altering the three-dimensional structure of the polypeptide, can reduce or inhibit the interaction between the host cell receptor and a viral protein. Similarly, decreasing, inhibiting or preventing expression of a host ligand polypeptide (or altering the structure of such a ligand) can decrease or inhibit an interaction between the viral protein and the
10 ligand. For example, decreasing or inhibiting expression of one or more enzymes involved in viral pathogenesis, such as those listed in Table 1 and those target sequences associated with SEQ ID NOS: 1-232, can block a component of the viral life cycle, such as blocking a signal pathway leading to transcription or translation of the viral genome, or assembly of viral sub-parts. Decreasing or inhibiting the enzymatic activity of an enzyme (rather than its expression) can have a similar effect.

Altering the nucleotide sequence of a host nucleic acid, for example by targeting disruption
15 of the nucleotide sequence using complementary nucleic acid sequences, can decrease, inhibit or prevent integration of a viral nucleic acid into the host nucleic acid. Methods that can be used to interrupt or alter translation of a host nucleic acid include, but are not limited to, using an antisense RNA, RNAi molecule, or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding a host polypeptide as described herein. Decreasing or inhibiting the expression of the host
20 nucleic acid can also alter the course of the disease. In one example, altering the nucleotide sequence of a host gene that is targeted by a virus for viral integration can decrease, inhibit, or even prevent, integration of that virus into the host genome.

A host nucleic acid involved in viral infection, including variants, fusions and fragments thereof, can be used to design agents that bind to a target sequence of that nucleic acid, such as
25 antisense nucleic acids or siRNAs. Such nucleic acid binding agents can be used to decrease or inhibit expression of the nucleic acid, to reduce the incidence of viral infection. For example, an expression vector that transcribes antisense RNA or siRNA that recognizes human β -chimerin mRNA is used to transform cell lines obtained from simians. These transformed cell lines are analyzed for infection by simian immunodeficiency virus (SIV), which is related to HIV. If those cells are
30 resistant to SIV infection, the disrupted gene is identified, sequenced, and compared to the human β -chimerin gene. Sequence similarities between the two genes will offer insight into common molecular mechanisms for infection by HIV and SIV, for example, common structural regions within their respective translated proteins.

A binding agent that recognizes a host nucleic acid involved in viral infection can be used
35 for prophylactic or therapeutic purposes. For example, expression vectors having antisense RNA, RNAi molecules, or siRNA molecules that target a host nucleic acid involved in viral infection, such as β -chimerin, are introduced into the bone marrow of a subject. Uptake of the vector and expression of the antisense RNA, RNAi, or siRNA within cells infected by HIV offers a prophylactic or therapeutic effect by disrupting the β -chimerin genes within those cells, thus decreasing or inhibiting

HIV infection. Similarly, expression vectors including Rab9 antisense RNA, RNAi, or siRNA molecules can be introduced into the bone marrow of a subject. Uptake of the vector and expression of Rab9 antisense RNA, RNAi, or siRNA within cells infected by a pathogen that can hijack a lipid raft, such as HIV or Ebola, offers a prophylactic or therapeutic effect by disrupting the Rab9 genes within those cells, thus decreasing or even inhibiting infection by a pathogen that can hijack a lipid raft. The vector, or other nucleic acid carrying the nucleic acid specific binding agent, is introduced into a subject by any standard molecular biology method and can be included in a composition containing a pharmaceutically acceptable carrier.

Decreasing or inhibiting the interaction between a viral protein and a host protein can decrease or inhibit viral infection. Methods that can be used to decrease an interaction between a viral protein and one or more host proteins (such as at least 2 host proteins, or at least 3 host proteins), include but are not limited to, disrupting expression of a host nucleic acid sequence encoding the host protein, (for example by functionally deleting the coding sequence, such as by a mutation, insertion, or deletion), altering the amino acid sequence or overall shape of the host protein, degrading the host protein, employing an agent that interferes with the viral protein or host protein (such as a specific binding agent, for example an antibody or small molecule), or a combination thereof.

For example, expression of a host protein can occur during transcription or translation of a nucleic acid encoding the host protein, or as a result of post-translational modification of a host protein. Methods that can be used to interrupt or alter transcription of a nucleic acid include, but are not limited to, site-directed mutagenesis, including mutations caused by a transposon or an insertional vector; and providing a DNA-binding protein that binds to the coding region of the host protein, thus blocking or interfering with RNA polymerase or another protein involved in transcription. Various inactive and recombinant DNA-binding proteins, and their effects on transcription, are discussed in Lewin, *Genes VII*. Methods that can be used to interrupt or alter translation of a nucleic acid include, but are not limited to, using an antisense RNA or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding the host polypeptide as described herein.

For example, exemplary host T-cell receptor polypeptides are encoded by target sequences associated with SEQ ID NOS: 1-20. Disrupting the expression of a nucleic acid including any target sequence associated with SEQ ID NOS: 1-20 can reduce or prevent production of the corresponding T-cell receptor polypeptide, and without access to the T-cell receptor polypeptide, an HIV virus cannot infect the host cell. Even if expression of the host nucleic acid is not completely blocked or disrupted, virus infection can still be inhibited. For example, interference with a host protein encoded by any target sequence associated with SEQ ID NOS: 1-20 reduces the number of T-cell receptors within that host cell available for recognition by an HIV virus, thus inhibiting HIV infection.

It is shown herein that inhibiting the interaction or activity between host Rab9 and HIV and Ebola using Rab9 siRNA molecules decreases infection of a host cell by the virus compared to the amount of infection in the absence of the siRNA molecules.

Host proteins involved in viral infection, such as those encoded by target cDNA sequences associated with SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 228, 230, and 232, can be used to generate specific binding agents to those proteins. The specific binding agent can be an anti-protein binding agent, such as a monoclonal or polyclonal antibody. Anti-protein binding agents can provide a prophylactic or therapeutic effect, for example by interfering with viral infection. Assays to determine whether an antibody interferes with viral infection are described herein. Antibodies that recognize a host protein involved in viral infection can prevent a virus or portion thereof (such as a viral protein) from binding to a host protein involved in viral infection. For example, a monoclonal or polyclonal antibody that binds to a V beta T-cell receptor on a cell can block the binding of HIV to that T-cell receptor, thus blocking infection of that cell. Effective amounts of such specific binding agents can be administered alone to a subject, or as part of a pharmaceutical composition, for the treatment of viral infection or as a prophylactic measure prior to the time the subject is exposed to the virus. In another example, specific binding agents that recognize a host protein involved in viral infection, such as β -chimerin or Rab9, can be used can be used to screen for the presence of the host protein, in other cells, tissues or lysates, including a biological sample obtained from a subject.

Host nucleic acids and polypeptides described herein, such as target sequences associated with SEQ ID NOS: 1-232, can be used for prophylactic or therapeutic uses. For example, polypeptides with structures mimicking a protein recognized by a virus can be administered to a subject as a pharmaceutical composition. These polypeptides interact with a virus already infecting that subject, or provide a prophylactic defense mechanism against infection if the subject is at risk of exposure to a virus. For example, polypeptides structurally similar to the T-cell receptor V beta 2.1 chain are recognized by HIV. If such polypeptides are administered to an HIV-positive subject, the viruses already present in the subject interact with those polypeptides in addition to that subject's T-cell receptors, thus inhibiting the rate at which HIV infects T-cells. The administered polypeptides act as "decoys" to block HIV from interacting with T-cell receptors. As another example, an agent that otherwise interferes with the interaction between a virus and a host protein can provide a similar prophylactic effect. For example, a chemical compound or anti-AMT binding agent (such as an antibody) that interferes with the interaction between AMT and an influenza virus (including an enzymatic inhibitor of AMT) provides a prophylactic or therapeutic effect against influenza A infection when provided to a host cell or administered to a host subject.

Additionally, the proteins described herein can be used to screen samples for the presence or absence of a particular antibody. For example, a β -chimerin or Rab9 protein can be used in an ELISA to screen a sample obtained from an individual for the presence of anti- β -chimerin or anti-Rab9 antibodies generated by that individual, such as a blood sample.

Using a method similar to that described for nucleic acid binding agents above, protein binding agents (such as agents that specifically bind β -chimerin, Rab9, or V beta T-cell receptor proteins) can be used to screen cells, individuals or populations for the presence or absence of

polypeptides related to infection (such as HIV, Ebola, or influenza infection), thus providing information about the susceptibility or resistance of that individual or population to viral infection.

The host nucleic acids, proteins, and related specific binding agents described herein can be used as models for the design of anti-viral drugs. For example, the three-dimensional structure of a protein described herein, such as β -chimerin, can be used in computer modeling of chemotherapeutic agents that block the activity of that moiety, for example by binding the protein. As another example, a monoclonal antibody can be used in a competitive binding assay to screen for other compounds that bind the same antigen.

Screening for Resistance to Infection

Also provided herein are methods of screening host subjects for resistance to infection by characterizing a nucleotide sequence of a host nucleic acid or the amino acid sequence of a host polypeptide (such as those shown in Table 1, or any target sequence associated with SEQ ID NOS: 1-232).

For example, the T-cell receptor V beta 2.1 chain nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20). The greater the similarity between that subject's V beta 2.1 chain nucleic acid and the sequence shown in SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20), the more susceptible that person is to HIV infection, while a decrease in similarity between that subject's V beta 2.1 chain nucleic acid and SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20), the more resistant that subject can be to HIV infection.

In another example, the aminomethyltransferase (AMT) nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37). The greater the similarity between that subject's AMT nucleic acid and the sequence shown in SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37), the more susceptible that person is to influenza A infection, while a decrease in similarity between that subject's AMT nucleic acid and SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37), the more resistant that subject can be to influenza A infection.

In yet another example, the Ras oncogene family member Rab9 nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119). The greater the similarity between that subject's Rab9 nucleic acid and the sequence shown in SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119), the more susceptible that person is to infection by a pathogen that uses lipid rafts, such as those listed in Table 2, while a decrease in similarity between that subject's Rab9 nucleic acid and SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119), the more resistant that subject may be to infection by a pathogen that uses lipid rafts.

Assessing the genetic characteristics of a population can provide information about the susceptibility or resistance of that population to viral infection. For example, polymorphic analysis of AMT alleles in a particular human population, such as the population of a particular city or

geographic area, can indicate how susceptible that population is to influenza A infection. A higher percentage of AMT alleles substantially similar to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that the population is more susceptible to influenza A infection, while a large number of polymorphic alleles that are substantially different than SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that a population is more resistant to influenza A infection. Such information can be used, for example, in making public health decisions about vaccinating susceptible populations.

Transgenic Cells and Non-Human Mammals

Transgenic animal models, including recombinant and knock-out animals, can be generated from the host nucleic acids described herein. Exemplary transgenic non-human mammals include, but are not limited to, mice, rats, chickens, cows, and pigs. In certain examples, a transgenic non-human mammal has a knock-out of one or more of the target sequences associated with SEQ ID NOS: 1-35, and has a decreased viral susceptibility, for example infection by HIV. In certain embodiments, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 36-63, and has a decreased viral susceptibility, for example infection by influenza A. In certain examples, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 64-232, and has a decreased viral susceptibility, for example infection by Ebola. In certain examples, a transgenic non-human mammal has a knock-out of any target sequence associated with SEQ ID NOS: 118-119, and has a decreased susceptibility to infection by a pathogen that uses a lipid raft, such as those listed in Table 2. Such knock-out animals are useful for reducing the transmission of viruses from animals to humans. In addition, animal viruses that utilize the same targets provided herein can be decreased in the animals.

Expression of the sequence used to knock-out or functionally delete the desired gene can be regulated by choosing the appropriate promoter sequence. For example, constitutive promoters can be used to ensure that the functionally deleted gene is never expressed by the animal. In contrast, an inducible promoter can be used to control when the transgenic animal does or does not express the gene of interest. Exemplary inducible promoters include tissue-specific promoters and promoters responsive or unresponsive to a particular stimulus (such as light, oxygen, chemical concentration, such as a tetracycline inducible promoter).

For example, a transgenic mouse including an AMT gene (such as a target sequence associated with SEQ ID NOS: 36-37), or a mouse having a disrupted AMT gene, can be examined during exposure to various mammalian viruses related to influenza A. Comparison data can provide insight into the life cycles of influenza and related viruses. Moreover, knock-out animals (such as pigs) that are otherwise susceptible to an infection (for example influenza) can be made to determine the resistance to infection conferred by disruption of the gene.

Transgenic pigs having a disrupted human protein tyrosine phosphatase gene can be produced and used as an animal model to determine other types of infections, including viral infections in mammals related to influenza A. A transgenic pig resistant to infection by viruses other

than influenza A is used to demonstrate the relatedness of influenza and those other viruses.

Transgenic animals, including methods of making and using transgenic animals, are described in various patents and publication, such as WO 01/43540; WO 02/19811; U.S. Pub. Nos: 2001-0044937 and 2002-0066117; and U.S. Pat. Nos: 5,859,308; 6,281,408; and 6,376,743; and the references cited therein.

Cells including an altered or disrupted host nucleic acid or polypeptide having a role in viral infection (such as a target sequence associated with SEQ ID NOS: 1-232), are resistant to infection by a virus (see Example 2). Such cells may therefore include cells having decreased susceptibility to HIV infection (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 1-35), Ebola infection (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 64-232), or influenza A (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 36-63). For example, cells in which a β -chimerin gene was disrupted using the gene-trap method remain CD4⁺ after HIV infection and do not produce further detectable HIV virus particles. Thus, disrupting the expression of β -chimerin can confer resistance on the cell to infection by HIV. Additionally, interfering with the activity of β -chimerin, such as contacting a β -chimerin with an enzymatic inhibitor or an anti- β -chimerin binding agent, can confer a similar resistance to HIV infection.

Screening for Agents that Decrease Viral Infection

A host nucleic acid or polypeptide involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, and peptides listed in Table 1, can be used to identify agents that inhibit the binding of a virus or viral protein to a host nucleic acid, a host protein, or another target protein capable of binding to the virus or viral protein. In some examples, a host molecule, such as a host protein or nucleic acid is contacted with a viral molecule, such as a virus or portion thereof, for example as a viral protein. One or more test agents are contacted with the host molecule, the viral molecule, both both molecules, before, during or after contacting the host and viral molecules. Subsequently, it is determined whether binding of the viral molecule to the host molecule is decreased in the presence of the test agent, wherein a decrease in binding is an indication that the test agent decreases the binding of viral protein to the target protein.

In other examples, a cell-based assay is used to identify proteins that decrease viral infection, for example using the yeast two-hybrid system.

For example, the binding of the T-cell receptor V-D-J beta 2.1 chain polypeptide to HIV (or an HIV envelope glycoprotein) can be determined in the presence of a test agent. A decrease in binding activity between the T-cell receptor V-D-J beta 2.1 chain polypeptide and HIV indicates that the test agent decreases the binding of HIV to the T-cell receptor V-D-J beta 2.1 chain, and the agent is a candidate for use as an anti-HIV agent. A decrease in binding activity can be determined by a comparison to a reference standard, such as a binding activity reported in the scientific literature, or to a control. Any suitable compound or composition can be used as a test agent, such as organic or inorganic chemicals, including aromatics, fatty acids, and carbohydrates; peptides, including

monoclonal antibodies, polyclonal antibodies, and other specific binding agents; or nucleic acids. The virus or viral molecule can be obtained from any suitable virus, such as HIV, influenza A, Ebola, and related viruses.

Therapeutic agents identified with the disclosed approaches can be used as lead compounds to identify other agents having even greater antiviral activity. For example, chemical analogs of identified chemical entities, or variant, fragments of fusions of peptide agents, are tested for their ability to decrease viral infection using the disclosed assays. Candidate agents are also tested for safety in animals and then used for clinical trials in animals or humans.

10 Microarrays

The host nucleic acids or proteins disclosed herein having a role in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, can be used in an array. The array can be a microarray, such as a nucleic acid array that includes probes to different polymorphic alleles of a human AMT gene (for example target sequence associated with SEQ ID NOS: 36-37) or a human Rab9 gene (for example target sequence associated with SEQ ID NOS: 118-119). Kits can be generated, such as diagnostic kits or kits for screening for the presence or absence of a host nucleic acid within a biological sample obtained from a subject or kits for administering an effective amount of a specific binding agent to a subject for a therapeutic or prophylactic purpose.

20 The following examples are provided to illustrate particular features of certain embodiments, but the scope of the claims should not be limited to those features exemplified.

Example 1

Generation of Cells with Increased Resistance to Viral Infection

25 The gene-trap method was used to identify cellular genes needed for viral propagation but whose inactivation is not lethal to the host cell. This was accomplished by using a Moloney murine leukemia virus-derived shuttle vector that encodes for a promoterless neomycin-resistance gene (FIG. 1). This vector integrates into the host genome at transcriptionally active genes, thereby disrupting the host gene but utilizing the host promoter to drive neomycin resistance carried by the vector. The cells are then infected with the desired virus. Cells surviving the viral infection carry an interrupted host gene that is needed during the viral life cycle. Since the construct is a shuttle vector, it can function as a plasmid and can be moved from mammalian to bacterial systems, facilitating subcloning and DNA sequencing. Using this approach, loci involved in, and in some cases required for viral infection, for example by HIV-1 and HIV-2, influenza A and Ebola virus were identified.

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Tissue culture

Sup-T1 human lymphoblastic leukemia cells were cultured in RPMI-1640 medium supplemented with 10% heat-inactivated fetal calf serum (FCS), penicillin, streptomycin and Fungisome. MDCK normal canine kidney cells were cultured in DMEM supplemented with 10%

fetal bovine serum (FBS), penicillin, streptomycin. Vero African green monkey kidney cells were cultured in DMEM supplemented with 10% FBS, amphotericin B, streptomycin, and Glutamine. All cultures were grown under 5% CO₂. Selection by all media was done in the presence of either 1 mg/ml (Sup-T1 and MDCK cells) or 400 mg/ml G418 (Geneticin; Vero cells).

5

Generation of gene-trapped library of cells

Parental, virus sensitive cells were plated and infected with U3neoSV1 as follows. Retrovirus vectors were obtained from H. Earl Ruley (Department of Microbiology and Immunology, Vanderbilt University School of Medicine, Nashville, TN). Stocks of the U3neoSV1 virus were prepared as described (Chen *et al.*, *Gene trap retroviruses in Methods in Molecular Genetics* (1994), page 123, herein incorporated by reference).

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FIG. 1 illustrates the U3neoSV1 retroviral vector, which contains a promoterless neomycin phosphotransferase gene (*Neo^R*) within the U3 unique sequence of the 5' long terminal repeat (LTR) of MMLV. Additionally, a second mutationally inactivated copy of *neo* is present in the 3' LTR. Portions of the MMLV genome were removed to impair replication, and were replaced with the β -lactamase gene which confers ampicillin resistance (*Amp^R*) to *E. coli* as well as an *E. coli* origin of replication (*ori*), flanked by two unique restriction sites for *Bam*HI (position 2570) and *Eco*RI (position 4175). Sites and orientations of primers used for sequence analysis of cloned genomic fragments are indicated by the triangular arrowheads.

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Parental, virus sensitive cells (106 Sup-T1 for HIV, Madin-Darby canine kidney, (MDCK) for influenza A, or Vero cells for Ebola) were plated for 12 hours before infection, after which U3neoSV1 was added at a multiplicity of infection (MOI) of 0.1, as titrated by adding 1 ml of diluted stocks to cultured cells in the presence of 4 μ g/ml polybrene. The cells were incubated at 37°C for one hour, 10 ml of fresh medium added, and the cells were incubated overnight at 37°C. The next day, the medium was replaced with the appropriate media containing 1 mg/ml G418 and maintained until surviving cells approached confluence, which was usually about two weeks.

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Upon random integration of the U3neoSV1 vector into the host genome, endogenous promoters result in expression of *Neo^R*, while expression of the exons 3' to the site of integration is disrupted. Therefore, only those events occurring at transcriptionally active promoters of non-essential genes are selected.

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A pool of the surviving cells, termed a library, including many cells bearing different disrupted genes was then exposed to the pathogen of interest. The resulting Sup-T1 library cells, MDCK library cells, and Vero library cells were infected HIV-1 and HIV-2; the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1); and Ebola, respectively, as follows.

35

An aliquot of the cell library was infected with three rounds of HIV-1 and three rounds of HIV-2 (3Bx in BC7 cells), normally a lethal event for Sup T-1 cells (FIG. 4). Approximately 3×10^8 actively growing Sup-T1 library cells were infected with the CXCR4 cytopathic HIV-1 strain LAI at an MOI of 10, approximately 100 fold greater than that normally used for spreading infection in culture. The cells were incubated with the virus for four hours in 2 ml of medium, then grown in bulk

at 10^6 cells/ml for two weeks, at which time G418 was added to a final concentration of 1 mg/ml and the cultures continued for an additional two weeks. The surviving cells were exposed to two further rounds of HIV-1 infection as described above and shown in FIG. 4.

Following HIV-1 infection, surviving cells were incubated 1:100 with BC7 T cells
5 constitutively expressing the HIV-2 strain 3BX, which was modified to infect regardless of CD4 status, solely using the CXCR4 receptor. Cells were coincubated for two weeks followed by selection with 1 mg/ml G418 (same as FIG. 4, but with HIV-2 instead of HIV-1). The surviving cells were exposed to two further rounds of HIV-2 infection.

The final cell culture was selected using anti-CD4 magnetic microbeads (Miltyni) and
10 divided into 2.0 ml cultures containing 1000 cells each. These were then infected with LAI at an MOI of 10. Surviving cells from each culture were subjected to limit dilution, or growth on methylcellulose, and expanded in selection medium. The isolated clones were identified as being CD4 and CXCR4 positive following flow cytometry analysis using standard protocols. Several cell isolates were resistant to further HIV infection with unique expression of CD4 cell surface antigen.

For influenza infection, approximately 10^7 actively growing MDCK library cells were
15 washed with phosphate buffered saline (Gibco) and infected with the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1) at an MOI of 20-30 in 250 μ l DMEM in a T-25 flask. The cells were incubated with the virus for two hours, and the inoculum was subsequently replaced with DMEM, supplemented with 2% FBS and 1 μ g/ml TPCK trypsin (to cleavage-activate
20 HA of new progeny virus). The cells were incubated for 18 hours to provide 2-3 rounds of infection. The maintenance medium was removed and replaced with selection medium (DMEM with 10% FBS and 1 mg/ml neomycin) and survivors allowed to expand. The surviving cells were exposed to one additional round of infection as described.

For filovirus infection, vero library cells were infected with either the Gulu 2000 or Zaire
25 1976 Ebola (EBO) strains, or the Voegelé 1967 strain of Marburg (MBG) at an MOI of greater than one in T-75 flasks in medium supplemented with 400 mg/ml G418. After a cytopathic effect (CPE) of 4+ was attained (greater than one week), survivors were harvested and reseeded undiluted and at 1:16 and 1:256 dilutions in selection medium. Wells with growth after 10 or more days were reinoculated into T12.5 flasks in selection medium and allowed to expand.

30 Cells surviving Ebola or influenza infection were cloned by either limiting dilution or growth on methylcellulose. The isolates were characterized phenotypically by flow cytometry and the interrupted gene determined by inverse PCR, cloning into BAC, or by the use of the shuttle feature of the vector followed by DNA sequence analysis.

35

Example 2

Cloning and Sequencing of Trapped Genes

This example describes the methods used to clone the sequences conferring resistance to the library of cells surviving viral infection. The identified sequences (SEQ ID NOS: 1-227, 229, 231)

encode host proteins that are involved in pathogen infection, and in some cases are required for the infectivity by the pathogen.

Isolation of trapped genes

5 The genomic DNA from actively growing virus-resistant isolates was extracted, prepared, and electroporated into cells as follows. Cellular DNA from actively growing virus-resistant isolates was extracted from one million cells using the QIAamp DNA Blood Mini Kit (Qiagen, Inc.) according to the manufacturer's instructions. Genomic DNA was digested at a final concentration of 150 µg/ml with either *EcoRI* or *BamHI* (New England Biolabs) at 1.5 or 2 units/µl, respectively (see
10 FIG. 1). Digested DNA was ethanol precipitated using oyster glycogen (Sigma) as a carrier, resuspended to a final concentration of 60 ng/µl and ligated using T4 DNA ligase (New England Biolabs). Genomic digestion resulted in the fragmentation of the retrovirus and the genomic DNA. Ligations were subsequently ethanol precipitated in the presence of glycogen, resuspended in 3 µl water and used directly to transform *E. coli*.

15 A 1.5 µl aliquot of each precipitated ligation was added to thawed Genehog cells (Invitrogen) or SURE cells (Stratagene), electroporated using a GenePulser (BioRad) according to the manufacturer's instructions, and plated onto Luria broth (LB) agar (1% tryptone, 0.5% yeast extract, 0.5% NaCl, 2% agar) containing 100 µg/µl carbenicillin (Sigma). Clones were isolated after 24 hours and used to inoculate 3 ml LB containing 100 µg/µl carbenicillin. Plasmid DNA was prepared after
20 overnight growth using the QIAprep Spin Miniprep Kit (QIAGEN, Inc.) according to the manufacturer's instructions and eluted in water.

Sequencing of Shuttle Clones

25 Due to the position of the unique sites in U3neoSV1, *BamHI* digestion facilitates cloning of DNA 3' to the site of integration, while *EcoRI* digestion results in the cloning of genomic DNA 5' to the site of integration. Using oligonucleotides homologous to the U3neoSV1 fragment, the sequence of the disrupted genomic DNA flanking the gene-trap insertion site was determined as follows.

 Sequencing reactions were performed using the ABI BigDye terminator cycle sequencing kit with reaction products resolved on either an ABI 3100 Genetic Analyzer or an ABI 377 DNA
30 Sequencer (Applied Biosystems, Foster City, CA). Sequences were obtained by using oligonucleotides 5'-ATCTTGTTC AATCATGCG (SEQ ID NO: 235) and 5'-GGGTCTGACGCTCATG (SEQ ID NO: 236) for *EcoRI*-generated shuttle clones, or 5'-GATAGGTGCCTCACTG (SEQ ID NO: 237) for *BamHI*-generated shuttle clones.

Sequence analysis

35 Sequences obtained from shuttle clones were analyzed by the Repeatmasker Web Server, available on the Internet at the website for the Department of Molecular Biotechnology, University of Washington, followed by standard nucleotide-nucleotide BLAST (blastn) against the National Center for Biotechnology Information databases, including nr (non-redundant

GenBank+EMBL+DDBJ+PDB sequences), est (expressed sequence tags) and htgs (unfinished High Throughput Genomic Sequences: phases 0, 1 and 2). Additionally, a nucleotide-protein database (blastx) analysis was performed against the nr database.

5 *Candidate Host Genes Required for Pathogenesis*

Candidate host genes required for the indicated pathogen, which were cloned via the gene-trap method and sequenced, are presented in Table 1 and in SEQ ID NOS: 1-226. The CD4⁺, latently infected, noninfectious HIV-resistant isolates 18B, 18E, 2B, and 2E were used to recover the genes involved in HIV-1 and HIV-2 pathogenesis, influenza A-resistant isolates B1, B3, B5, B6, and B7
10 were used to recover the host genes involved in influenza A pathogenesis, and Ebola-resistant isolates ZV and MV were used to recover the host genes involved in Ebola pathogenesis. Candidate genes can be validated by siRNA and cDNA complementation, as described in Example 3.

In summary, using the U3neoSV1 gene-trap, sixteen HIV-1 and -2 resistant Sup-T1 cell lines, and fifteen influenza A resistant MDCK cell lines were isolated and characterized. Twenty-
15 three EBO-Zaire resistant Vero cell line pools, twenty-four EBO-Gulu resistant pools, and thirty MBG resistant pools were screened. The shuttle-vector design of the U3neoSV1 gene-trap allowed identification of multiple host genes involved in the pathogenesis of HIV-1, HIV-2, influenza A, and Ebola, which are described herein and summarized in Table 1 and sequences provided in SEQ ID NOS: 1-232. Cross-resistance of resistant isolates to multiple pathogens can be quickly examined to
20 reveal common pathways in the viral life cycles.

Example 3

siRNA Molecules Decrease Viral Infection

This example describes methods used to express siRNAs that recognize Rab9 (such as a
25 target sequence associated with SEQ ID NOS: 118-119), AXL (AXL receptor tyrosine kinase; such as a target sequence associated with SEQ ID NO: 226), CHN (beta-chimerin; such as a target sequence associated with SEQ ID NOS: 21-22), KOX (such as a target sequence associated with SEQ ID NO: 30), RBB (retinoblastoma binding protein 1; such as a target sequence associated with SEQ ID NOS: 120-122), KIAA1259; F3 (such as a target sequence associated with SEQ ID NO: 29), and
30 Mselb (mammalian selenium binding protein; such as a target sequence associated with SEQ ID NO: 124).

The following Rab9 siRNA sequences were generated by Dharmacon, RNA Technologies (Lafayette, CO) using chemical synthesis: GGGAAGAGTTCACTTATGA (SEQ ID NO: 238); TCACAAAGCTTCCAGAACT (SEQ ID NO: 239); GTAACAAGATTGACATAAG (SEQ ID NO: 240); and GGAAGTGGATGGACATTTT (SEQ ID NO: 241).
35

The following AXL (AXL receptor tyrosine kinase) siRNA sequences were generated by Dharmacon, RNA Technologies using chemical synthesis: GGUCAGAGCUGGAGGAUUU (SEQ ID NO: 242); GAAAGAAGGAGACCCGUUA (SEQ ID NO: 243);

CCAAGAAGAUCUACAAUGG (SEQ ID NO: 244); and GGAACUGCAUGCUGAAUGA (SEQ ID NO: 245).

5 siRNA sequences were also used that recognized CHN (beta-chimerin); KOX (similar to KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); KIAA1259; F3 and mammalian selenium binding protein. One skilled in the art will understand that siRNA sequences that recognize other sequences involved in viral infection (such as a target sequence associated with any of SEQ ID NOS: 1-232) can be designed and prepared by commercial entities, such as Dharmacon, RNA Technologies.

10 The four siRNA sequences for each gene (CHN, KOX, RBB, RAB, KIAA1259, F3, ASL and Mselb) were separately pooled. Each of the eight pools of siRNAs, hybridized to its appropriate complement sequence, were used to transfect JC53 (HeLa cells modified to accept HIV), Vero (monkey kidney cells), MDCK (dog kidney cells), or HEK (human kidney cells). All cells were obtained from American Type Culture Collection (ATCC, Manassas, VA). GFP siRNA sequences were used as a negative control.

15 Cells (20,000 to 250,000) were incubated in serum free media for 24 hours. Cocktails were made by mixing the appropriate duplex siRNAs (50-100 pmoles) with lipofectamine 2000 (4-16 μ l) and RNase Inhibitor (1-4 μ l) in a solution of Optimem (serum free medium) in a total volume of 200-2000 μ l. The lipofectamine was allowed to incubate at room temperature for 5 minutes before the addition of siRNA. Aliquots (50-500 μ l) of the cocktail were added to the cells which were 20 incubated at 37°C for 48 hours. The cells were then infected with HIV, Ebola, or influenza and the incubation continued for 3-7 days. Following transfection, several assays were conducted to confirm transfection efficiency, and to determine the resistance of the cells to infection by various agents.

Quantitation of p24 levels in HIV infected JC53 cells was determined using the Coulter HIV-1 p24 Antigen Neutralization Kit according to the manufacturers recommendation. As shown in 25 FIG. 5, Rab9 siRNAs and mammalian selenium binding protein siRNAs each decreased HIV infection by about 50% on day 4 post infection (day 7 post addition of siRNA). In addition, HIV infection decreased by about 80-90% in the presence of beta-chimerin siRNAs, KOX (similar to KOX4 (LOC131880) and LOC166140) siRNAs, or retinoblastoma binding protein 1 siRNAs. However, HIV infection did not decrease in the presence of siRNAs that recognize KIAA1259, tissue 30 factor 3, or AXL receptor tyrosine kinase. It is possible that apoptosis is interrupted by the siRNAs, so the cell lives through the infection but still makes virus. It is also possible that the p24 levels are elevated but is not associated with infectious particles.

To determine the level of Ebola infection in HEK293 cells transfected with Rab9 or AXL siRNA, the presence of gp1 antigen was determined by using a fluorescent antibody to gp1 envelope 35 protein. Infection by Ebola decreased by at least about 90-95% in the presence of Rab9 siRNA, as compared to the amount of infection in the absence of Rab9 siRNA. Infection by Ebola decreased by at least about 80% in the presence of AXL siRNA, as compared to the amount of infection in the absence of AXL siRNA.

Example 4

Expression of Rab9 siRNA Decreases Lipid Raft Formation

As described in Example 3, siRNA molecules that recognize Rab9 decrease viral infection. Rab9 transports late endosomes to trans-golgi. Based on these results, a model is proposed whereby Rab9 plays a role in lipid raft formation (FIG. 6). Lipid rafts are liquid-ordered microdomains enriched in sphingolipids and cholesterol, and are involved in biosynthetic traffic, signal transduction, and endocytosis. Viruses take advantage of ("hijack") rafts for completion of some steps of their replication cycle, such as entry into their cell host, assembly, and budding. Without wishing to be bound to a particular theory, it is proposed that Rab9 trafficks cholesterol, the dynamic glue that holds lipid rafts together. Further evidence for this hypothesis is based on observations of Neimann-Pick type C disease cells. Neimann-Pick type C is a genetic disease that results in accumulation of abnormally high levels of intracellular cholesterol. However, over expression of Rab9 in Neimann-Pick type C disease cells, decreases the level of cholesterol.

Examples of pathogens that hijack lipid rafts include, but are not limited to those shown in Table 2. In the absence of functional Rab9 and lipid rafts (or a decrease in the number of rafts), viruses may not be able to bud or be infectious. Therefore, the use of agents that decrease or inhibit Rab9 expression or activity can be used to decrease infection by other pathogens, as well as toxins such as anthrax, that hijack lipid rafts, such as those shown in Table 2.

Table 2: Pathogens that hijack lipid rafts.

| Intracellular survival | Bacteria | | Viruses | Protozoa |
|-------------------------------------|-------------------------------|--|----------------------------------|------------------------------|
| | Toxin binding/oligomerization | | | |
| <i>Campylobacter jejuni</i> | <i>Vibrio cholerae</i> | | SV40 | <i>Toxoplasma gondii</i> |
| <i>Legionella pneumophila</i> | <i>Aeromonas hydrophila</i> | | Echovirus 1 and 11 | <i>Plasmodium falciparum</i> |
| <i>Brucella spp</i> | <i>Clostridium spp.</i> | | Avian sarcoma and leukosis virus | |
| <i>FimH and Dr Escherichia coli</i> | <i>Streptococcus pyogenes</i> | | Semiliki forest virus | |
| <i>Salmonella typhimurium</i> | <i>Bacillus anthracis</i> | | Ecotropic mouse leukaemia virus | |
| <i>Shigella flexneri</i> | <i>Bacillus thuringiensis</i> | | HTLV-1 | |
| <i>Chlamydia spp.</i> | <i>Helicobacter pylori</i> | | HIV-1 | |
| <i>Mycobacterium spp.</i> | <i>Lysteria monocytogenes</i> | | Ebola and Marburg viruses | |
| | | | Measles virus | |
| | | | Herpes Simplex virus | |
| | | | Influenza virus | |
| | | | Epstein-Barr virus | |

This example therefore illustrates that identification of an agent (such as a small molecule or siRNA) that inhibits a particular pathogen can be used to inhibit other pathogens that have a similar mechanism of action.

Example 5

RNAi Molecules

This example describes methods that can be used to decrease or inhibit expression of any of the genes listed in Table 1, or target sequences associated with SEQ ID NOS: 1-232, to decrease viral infection, such as infection by HIV, Ebola, or influenza. Exemplary RNAi compounds are provided for several different genes, such as beta-chimerin receptor tyrosine kinase, retinoblastoma binding protein 1, *Homo sapiens* chromosome 10 open reading frame 3, *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*), transcript variant 1, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3), malic enzyme, cadherin related 23, sideroflexin 5, polybromo 1, elongation factor for selenoprotein translation, integrin, beta 1, huntingtin interacting protein 1 and cyclin M2.

One skilled in the art will understand that RNAi molecules can be generated to any of the genes listed in Table 1. Although only 27mers are shown in SEQ ID NOS: 246-845, this disclosure is not limited to RNAi compounds of a particular length. An RNAi molecule can be any length, such as at least about 25 nucleotides, or even as many as 400 nucleotides. One skilled in the art will also understand that RNAi sequences that recognize other sequences involved in viral infection (such as a target sequence associated with any of SEQ ID NOS: 1-232) can be designed and prepared by commercial entities, such as Sequitur, Inc. (Natick, MA).

Using the methods described in Example 3, the disclosed RNAi compounds are used to decrease viral infection. For example, a 27mer RNAi compound shown in any of SEQ ID NOS: 246-845 is incubated with its reverse complement, allowing hybridization of the two molecules. In particular examples, two or more, such as three or more, 27mer RNAi compounds are transfected into a cell. This duplex molecule is contacted with a cell, such as a cell of a subject in whom decreased viral infection is desired, under conditions that allow the duplex to enter the cell.

Example 6

Disruption of Gene Expression

This example describes methods that can be used to disrupt expression of a host gene, such as those shown in Table 1 and target sequences associated with SEQ ID NOS: 1-232, and thereby decrease activity of the proteins encoded by these sequences. Such methods are useful when it is desired to decrease or inhibit viral infection. In a particular example, disrupted expression of at least one target sequence associated with SEQ ID NOS: 1-232 in a host cell is used to treat a subject having a viral infection, or susceptible to a viral infection. Methods useful for disrupting gene function or expression are the use of antisense oligonucleotides, siRNA molecules (see Example 3), RNAi molecules (see Example 5), ribozymes, and triple helix molecules. Techniques for the production and use of such molecules are well known to those of skill in the art.

Antisense Methods

To design antisense oligonucleotides, a host mRNA sequence is examined. Regions of the sequence containing multiple repeats, such as TTTTTTTT, are not as desirable because they will lack specificity. Several different regions can be chosen. Of those, oligos are selected by the following characteristics: those having the best conformation in solution; those optimized for hybridization characteristics; and those having less potential to form secondary structures. Antisense molecules having a propensity to generate secondary structures are less desirable.

Plasmids including antisense sequences that recognize one or more of the target sequences associated with SEQ ID NOS: 1-232 (such as a sequence that encodes a protein listed in Table 1) can be generated using standard methods. For example, cDNA fragments or variants coding for a host protein involved in viral infection are PCR amplified. The nucleotides are amplified using Pfu DNA polymerase (Stratagene) and cloned in antisense orientation a vector, such as pcDNA vectors (InVitrogen, Carlsbad, CA). The nucleotide sequence and orientation of the insert can be confirmed by sequencing using a Sequenase kit (Amersham Pharmacia Biotech).

Generally, the term "antisense" refers to a nucleic acid capable of hybridizing to a portion of a host RNA sequence (such as mRNA) by virtue of some sequence complementarity. The antisense nucleic acids disclosed herein can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

Antisense nucleic acids are polynucleotides, and can be oligonucleotides (ranging from about 6 to about 100 oligonucleotides). In one example, an antisense polynucleotide recognizes one or more of the target nucleic acid sequences associated with SEQ ID NOS: 1-227, 229, or 231. In specific examples, the oligonucleotide is at least 10, 15, or 100 nucleotides, or a polynucleotide of at least 200 nucleotides. However, antisense nucleic acids can be much longer. The nucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, and can include other appending groups such as peptides, or agents facilitating transport across the cell membrane (Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 1989, 86:6553-6; Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 1987, 84:648-52; WO 88/09810) or blood-brain barrier (WO 89/10134), hybridization triggered cleavage agents (Krol *et al.*, *BioTechniques* 1988, 6:958-76) or intercalating agents (Zon, *Pharm. Res.* 5:539-49, 1988).

An antisense polynucleotide (including oligonucleotides) that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can be modified at any position on its structure with substituents generally known in the art. For example, a modified base moiety can be 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N-6-sopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-

oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-S-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine.

5 An antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can include at least one modified sugar moiety such as arabinose, 2-fluoroarabinose, xylose, and hexose, or a modified component of the phosphate backbone, such as phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, or a formacetal or analog thereof.

10 In a particular example, an antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, *Nucl. Acids Res.* 15:6625-41, 1987). The oligonucleotide can be conjugated to another molecule, such as a
15 peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent. Oligonucleotides can include a targeting moiety that enhances uptake of the molecule by host cells. The targeting moiety can be a specific binding molecule, such as an antibody or fragment thereof that recognizes a molecule present on the surface of the host cell.

Polynucleotides disclosed herein can be synthesized by standard methods, for example by
20 use of an automated DNA synthesizer. As examples, phosphorothioate oligos can be synthesized by the method of Stein *et al.* (*Nucl. Acids Res.* 1998, 16:3209), methylphosphonate oligos can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, *Proc. Natl. Acad. Sci. USA* 85:7448-51, 1988). In a specific example, antisense oligonucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 includes catalytic RNA, or a
25 ribozyme (see WO 90/11364, Sarver *et al.*, *Science* 247:1222-5, 1990). In another example, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, *Nucl. Acids Res.* 15:6131-48, 1987), or a chimeric RNA-DNA analogue (Inoue *et al.*, *FEBS Lett.* 215:327-30, 1987).

The antisense polynucleic acids disclosed herein include a sequence complementary to at least a portion of an RNA transcript of a gene, such as a target sequence associated with SEQ ID
30 NOS: 1-227, 229, or 231. However, absolute complementarity, although advantageous, is not required. A sequence can be complementary to at least a portion of an RNA, meaning a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation can be assayed. The ability to hybridize depends on the degree of
35 complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The relative ability of polynucleotides (such as oligonucleotides) to bind to complementary strands is compared by determining the T_m of a hybridization complex of the poly/oligonucleotide and its complementary strand. The higher the T_m the greater the strength of the binding of the hybridized strands. As close to optimal fidelity of base pairing as possible achieves optimal
5 hybridization of a poly/oligonucleotide to its target RNA.

The amount of antisense nucleic acid that is effective in the treatment of a particular disease or condition (the therapeutically effective amount) depends on the nature of the disease or condition, and can be determined by standard clinical techniques. For example, it can be useful to use compositions to achieve sustained release of an antisense nucleic acid, for example an antisense
10 molecule that recognizes one or more target sequences associated with SEQ ID NOS: 1-227, 229, or 231. In another example, it may be desirable to utilize liposomes targeted via antibodies to specific cells.

As an alternative to antisense inhibitors, catalytic nucleic acid compounds, such as ribozymes or anti-sense conjugates, can be used to inhibit gene expression. Ribozymes can be
15 synthesized and administered to the subject, or can be encoded on an expression vector, from which the ribozyme is synthesized in the targeted cell (as in WO 9523225, and Beigelman *et al. Nucl. Acids Res.* 1995, 23:4434-42). Examples of oligonucleotides with catalytic activity are described in WO 9506764. Conjugates of antisense with a metal complex, such as terpyridylCu (II), capable of mediating mRNA hydrolysis, are described in Bashkin *et al. (Appl. Biochem Biotechnol.* 54:43-56,
20 1995).

Ribozymes

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme
25 molecule to complementary target RNA, followed by an endonucleolytic cleavage. Methods of using ribozymes to decrease or inhibit RNA expression are known in the art. An overview of ribozymes and methods of their use is provided in Kashani-Sabet (*J. Investig. Dermatol. Symp. Proc.*, 7:76-78, 2002).

Ribozyme molecules include one or more sequences complementary to the target host mRNA and include the well-known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246, herein incorporated by reference).

A ribozyme gene directed against any of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 can be delivered to a subject endogenously (where the ribozyme coding gene is transcribed intracellularly) or exogenously (where the ribozymes are introduced into a cell, for
35 example by transfection). Methods describing endogenous and exogenous delivery are provided in Marshall *et al. (Cell Mol. Neurobiol.* 14:523-38, 1994).

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites that include the following sequence: GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and ribonucleotides

corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

For example, a plasmid that contains a ribozyme gene directed against a β -chimerin rho-GTPase, placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to HIV infection. Expression of this plasmid in a cell will decrease or inhibit β -chimerin rho-GTPase RNA expression in the cell. In another example, a plasmid that contains a ribozyme gene directed against Rab9 placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to infection by a pathogen that utilizes lipid rafts, such as Ebola. Expression of this plasmid in a cell will decrease or inhibit Rab9 RNA expression in the cell. Other examples of using ribozymes to decrease or inhibit RNA expression can be found in WO 01/83754 (herein incorporated by reference).

Triple helix molecules

Nucleic acid molecules used in triplex helix formation should be single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is ideally designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, contain a stretch of guanidine residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with one strand of a duplex first and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Example 7

Methods of Treatment

When the activity of a host cell protein or nucleic acid involved in viral infection is decreased by prematurely downregulating their levels of expressing using antisense molecules, a reduction in viral infection can be achieved. Antisense oligonucleotides, RNAi molecules, ribozymes, and siRNA molecules that recognize a host nucleic acid involved in viral infection

(Example 6) can therefore be used to disrupt cellular expression of a host protein involved in viral infection. The disclosed antisense, ribozyme, RNAi molecules and siRNA molecules can be administered to a subject alone, or in combination with other therapeutic agents such as anti-viral compounds.

5 A subject susceptible to or suffering from a viral infection, wherein decreased amounts of infection by the virus is desired, can be treated with a therapeutically effective amount of antisense, ribozyme, RNAi molecule or siRNA molecule (or combinations thereof) that recognizes a host sequence involved in viral infection, such as those shown in Table 1 or target sequences associated with SEQ ID NOS: 1-232. After the antisense, ribozyme, RNAi molecule or siRNA molecule has
10 produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for diseases associated with viral infection.

 Similarly, other agents, such as an antibody that recognizes a host protein involved in viral infection and prevents the protein from interacting with a viral protein, can also be used to decrease
15 or inhibit viral infection. Other exemplary agents are those identified using the methods described in the Examples below. These agents, such as antibodies, peptides, nucleic acids, organic or inorganic compounds, can be administered to a subject in a therapeutically effective amount. After the agent has produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for
20 diseases associated with viral infection.

 The treatments disclosed herein can also be used prophylactically, for example to inhibit or prevent a viral infection. Such administration is indicated where the treatment is shown to have utility for treatment or prevention of the disorder. The prophylactic use is indicated in conditions known or suspected of progressing to disorders associated with a viral infection.

25

Example 8

Recombinant Expression

 With the disclosed host sequences involved in viral infection, native and variant sequences can be generated. Expression and purification by standard laboratory techniques of any variant, such
30 as a polymorphism, mutant, fragment or fusion of a sequence involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, is enabled. One skilled in the art will understand that the sequences involved in viral infection, as well as variants thereof, can be produced recombinantly in any cell or organism of interest, and purified prior to use.

 Methods for producing recombinant proteins are well known in the art. Therefore, the scope
35 of this disclosure includes recombinant expression of any host protein or variant or fragment thereof involved in viral infection. For example, see U.S. Patent No: 5,342,764 to Johnson *et al.*; U.S. Patent No: 5,846,819 to Pausch *et al.*; U.S. Patent No: 5,876,969 to Fleer *et al.* and Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989, Ch. 17, herein incorporated by reference).

Briefly, partial, full-length, or variant cDNA sequences that encode for a protein involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, can be ligated into an expression vector, such as a bacterial expression vector. Proteins or peptides can be produced by placing a promoter upstream of the cDNA sequence. Examples of promoters include, but are not
5 limited to *lac*, *trp*, *tac*, *trc*, major operator and promoter regions of phage lambda, the control region of fd coat protein, the early and late promoters of SV40, promoters derived from polyoma, adenovirus, retrovirus, baculovirus and simian virus, the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, the promoter of the yeast alpha-mating factors and combinations thereof.

10 Vectors suitable for the production of intact proteins include pKC30 (Shimatake and Rosenberg, 1981, *Nature* 292:128), pKK177-3 (Amann and Brosius, 1985, *Gene* 40:183) and pET-3 (Studiar and Moffatt, 1986, *J. Mol. Biol.* 189:113). A DNA sequence can be transferred to other cloning vehicles, such as other plasmids, bacteriophages, cosmids, animal viruses and yeast artificial chromosomes (YACs) (Burke *et al.*, 1987, *Science* 236:806-12). These vectors can be introduced
15 into a variety of hosts including somatic cells, and simple or complex organisms, such as bacteria, fungi (Timberlake and Marshall, 1989, *Science* 244:1313-7), invertebrates, plants (Gasser and Fraley, 1989, *Science* 244:1293), and mammals (Pursel *et al.*, 1989, *Science* 244:1281-8), that are rendered transgenic by the introduction of the heterologous cDNA.

For expression in mammalian cells, a cDNA sequence, such as a coding sequence of any
20 target sequence associated with SEQ ID NOS: 1-227, 229, or 231, can be ligated to heterologous promoters, such as the simian virus SV40, promoter in the pSV2 vector (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6), and introduced into cells, such as monkey COS-1 cells (Gluzman, 1981, *Cell* 23:175-82), to achieve transient or long-term expression. The stable integration of the chimeric gene construct may be maintained in mammalian cells by biochemical
25 selection, such as neomycin (Southern and Berg, 1982, *J. Mol. Appl. Genet.* 1:327-41) and mycophenolic acid (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6).

The transfer of DNA into eukaryotic, such as human or other mammalian cells is a conventional technique. The vectors are introduced into the recipient cells as pure DNA (transfection) by, for example, precipitation with calcium phosphate (Graham and vander Eb, 1973, *Virology* 52:466) strontium phosphate (Brash *et al.*, 1987, *Mol. Cell Biol.* 7:2013), electroporation (Neumann *et al.*, 1982, *EMBO J.* 1:841), lipofection (Felgner *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:7413), DEAE dextran (McCuthan *et al.*, 1968, *J. Natl. Cancer Inst.* 41:351), microinjection (Mueller *et al.*, 1978, *Cell* 15:579), protoplast fusion (Schafner, 1980, *Proc. Natl. Acad. Sci. USA* 77:2163-7), or pellet gums (Klein *et al.*, 1987, *Nature* 327:70). Alternatively, the cDNA can be
35 introduced by infection with virus vectors, for example retroviruses (Bernstein *et al.*, 1985, *Gen. Engrg.* 7:235) such as adenoviruses (Ahmad *et al.*, *J. Virol.* 57:267, 1986) or Herpes (Spaete *et al.*, *Cell* 30:295, 1982).

Pharmaceutical Compositions and Modes of Administration

Various delivery systems for administering the therapies disclosed herein are known, and include encapsulation in liposomes, microparticles, microcapsules, expression by recombinant cells, receptor-mediated endocytosis (Wu and Wu, *J. Biol. Chem.* 1987, 262:4429-32), and construction of therapeutic nucleic acids as part of a retroviral or other vector. Methods of introduction include, but are not limited to, topical, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, and oral routes. The compounds can be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (for example, oral mucosa, rectal, vaginal and intestinal mucosa, etc.) and can be administered together with other biologically active agents. Administration can be systemic or local. Pharmaceutical compositions can be delivered locally to the area in need of treatment, for example by topical application.

Pharmaceutical compositions are disclosed that include a therapeutically effective amount of an RNA, DNA, antisense molecule, ribozyme, RNAi molecule, siRNA molecule, specific-binding agent, or other therapeutic agent, alone or with a pharmaceutically acceptable carrier. Furthermore, the pharmaceutical compositions or methods of treatment can be administered in combination with (such as before, during, or following) other therapeutic treatments, such as other antiviral agents.

Delivery systems

The pharmaceutically acceptable carriers useful herein are conventional. *Remington's Pharmaceutical Sciences*, by Martin, Mack Publishing Co., Easton, PA; 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of the therapeutic agents herein disclosed. In general, the nature of the carrier will depend on the mode of administration being employed. For instance, parenteral formulations usually include injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, sesame oil, glycerol, ethanol, combinations thereof, or the like, as a vehicle. The carrier and composition can be sterile, and the formulation suits the mode of administration. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. For solid compositions (for example powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, sodium saccharine, cellulose, magnesium carbonate, or magnesium stearate. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides.

Embodiments of the disclosure including medicaments can be prepared with conventional pharmaceutically acceptable carriers, adjuvants and counterions as would be known to those of skill in the art.

5 The amount of therapeutic agent effective in decreasing or inhibiting viral infection can depend on the nature of the virus and its associated disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* assays can be employed to identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Effective doses can be extrapolated
10 from dose-response curves derived from *in vitro* or animal model test systems.

The disclosure also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by
15 the agency of manufacture, use or sale for human administration. Instructions for use of the composition can also be included.

Administration of Nucleic Acids

In an example in which a nucleic acid is employed to reduce viral infection, such as an
20 antisense, RNAi molecule, or siRNA molecule, the nucleic acid can be delivered intracellularly (for example by expression from a nucleic acid vector or by receptor-mediated mechanisms), or by an appropriate nucleic acid expression vector which is administered so that it becomes intracellular, for example by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (such as a gene gun; Biolistic, Dupont), or coating with lipids or cell-
25 surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (for example Joliot *et al.*, *Proc. Natl. Acad. Sci. USA* 1991, 88:1864-8). The present disclosure includes all forms of nucleic acid delivery, including synthetic oligos, naked DNA, plasmid and viral, integrated into the genome or not.

30

Example 10

***in vitro* Screening Assay for Agents that Decrease Viral Infection**

This example describes *in vitro* methods that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. As disclosed in the Examples above, the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof) are involved
5 in viral infection (such as infection by HIV, Ebola, and influenza A), and the host protein/viral protein interaction is a component in the ability of a virus to infect a cell. Therefore, screening assays can be used to identify and analyze agents that decrease or interfere with this interaction. For example, the following assays can be used to identify agents that interfere with the interaction of the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated
10 with SEQ ID NOS: 1-232) with a viral protein sequence. However, the present disclosure is not limited to the particular methods disclosed herein.

Agents identified via the disclosed assays can be useful, for example, in decreasing or even inhibiting viral infection by more than an amount of infection in the absence of the agent, such as a decrease of at least about 10%, at least about 20%, at least about 50%, or even at least about 90%.
15 This decrease in viral infection can serve to ameliorate symptoms associated with viral infection, such as fever. Assays for testing the effectiveness of the identified agents, are discussed below.

Exemplary test agents include, but are not limited to, any peptide or non-peptide composition in a purified or non-purified form, such as peptides made of D-and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam *et al.*, *Nature* 354:82-4,
20 1991), phosphopeptides (such as in the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang *et al.*, *Cell* 72:767-78, 1993), antibodies, and small or large organic or inorganic molecules. A test agent can also include a complex mixture or "cocktail" of molecules.

The basic principle of the assay systems used to identify agents that interfere with the
25 interaction between a host protein, such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, and its viral protein binding partner or partners, involves preparing a reaction mixture containing the host protein and a viral protein under conditions and for a time sufficient to allow the two proteins to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction is conducted in the presence and absence of the test
30 agent. The test agent can be initially included in the reaction mixture, or added at a time subsequent to the addition of a host protein and a viral protein. Controls are incubated without the test agent or with a placebo. Exemplary controls include agents known not to bind to viral or host proteins. The formation of any complexes between the host protein and the viral protein is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test
35 agent, indicates that the agent interferes with the interaction of the host protein and the viral protein, and is therefore possibly an agent that can be used to decrease viral infection.

The assay for agents that interfere with the interaction of host and viral proteins can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring the host protein or the viral protein onto a solid phase and detecting complexes anchored on the solid

phase at the end of the reaction. In some examples, the method further involves quantitating the amount of complex formation or inhibition. Exemplary methods that can be used to detect the presence of complexes, when one of the proteins is labeled, include ELISA, spectrophotometry, flow cytometry, and microscopy. In homogeneous assays, the entire reaction is performed in a liquid phase. In either method, the order of addition of reactants can be varied to obtain different information about the agents being tested. For example, test agents that interfere with the interaction between the proteins, such as by competition, can be identified by conducting the reaction in the presence of the test agent, for example by adding the test agent to the reaction mixture prior to or simultaneously with the host protein and viral protein. On the other hand, test agents that disrupt preformed complexes, such as agents with higher binding constants that displace one of the proteins from the complex, can be tested by adding the test agent to the reaction mixture after complexes have been formed. The various formats are described briefly below.

Once identified, test agents found to inhibit or decrease the interaction between a host protein and a viral protein can be formulated in therapeutic products (or even prophylactic products) in pharmaceutically acceptable formulations, and used for specific treatment or prevention of a viral disease, such as HIV, Ebola, or influenza A.

Heterogeneous assay system

In a heterogeneous assay system, one binding partner, either the host protein (such as those listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or the viral protein (such as an HIV, Ebola, or influenza A virus preparation) is anchored onto a solid surface (such as a microtiter plate), and its binding partner, which is not anchored, is labeled, either directly or indirectly. Exemplary labels include, but are not limited to, enzymes, fluorophores, ligands, and radioactive isotopes. The anchored protein can be immobilized by non-covalent or covalent attachments. Non-covalent attachment can be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody (such as a monoclonal antibody) specific for the protein can be used to anchor the protein to the solid surface. The surfaces can be prepared in advance and stored.

To conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test agent. After the reaction is complete, unreacted components are removed (such as by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; for example by using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test agent, the reaction products separated from unreacted components, and complexes detected; for example by using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test agents which inhibit complex or which disrupt preformed complexes can be identified.

Homogenous assays

In an alternate example, a homogeneous assay can be used. In this method, a preformed complex of the host protein and the viral protein is prepared in which one of the proteins is labeled, but the signal generated by the label is quenched due to complex formation (for example, see U.S. Pat. No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test agents that disrupt host protein-viral protein interactions are identified.

Immobilization of Proteins

In a particular example, a host protein involved in viral infection (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232) can be prepared for immobilization using recombinant DNA techniques. For example, a coding region of a protein listed in Table 1, or any target sequence associated with SEQ ID NOS: 1-232, can be fused to a glutathione-S-transferase (GST) gene using the fusion vector pGEX-5X-1, in such a manner that its binding activity is maintained in the resulting fusion protein. The viral protein (such as an Ebola, HIV, or influenza A protein or viral preparation) can be purified and used to raise a monoclonal antibody, using methods routinely practiced in the art and described above. This antibody can be labeled with the radioactive isotope ^{125}I using methods routinely practiced in the art.

In a heterogeneous assay, for example, the GST-host fusion protein can be anchored to glutathione-agarose beads. The viral protein preparation can then be added in the presence or absence of the test agent in a manner that allows interaction and binding to occur. At the end of the reaction period, unbound material can be washed away, and the labeled monoclonal antibody can be added to the system and allowed to bind to the complexed binding partners. The interaction between the host protein and the viral protein can be detected by measuring the amount of radioactivity that remains associated with the glutathione-agarose beads. A successful inhibition of the interaction by the test compound will result in a decrease in measured radioactivity.

Alternatively, the GST-host fusion protein and the viral protein can be mixed together in liquid in the absence of the solid glutathione agarose beads. The test agent can be added either during or after the binding partners are allowed to interact. This mixture can then be added to the glutathione-agarose beads and unbound material is washed away. Again, the extent of inhibition of

the binding partner interaction can be detected by adding the labeled antibody and measuring the radioactivity associated with the beads.

In another example, these same techniques can be employed using peptide fragments that correspond to the binding domains of the host protein and the viral protein, respectively, in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the protein's binding site. These methods include, but are not limited to, mutagenesis of one of the genes encoding the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in a host gene can be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in above, and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the for the cellular or extracellular protein is obtained, short gene segments can be engineered to express peptide fragments of the protein, which can then be tested for binding activity and purified or synthesized.

For example, a host protein can be anchored to a solid material as described above by making a GST-host protein fusion protein and allowing it to bind to glutathione agarose beads. The viral protein can be labeled with a radioactive isotope, such as ^{35}S , and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-host protein fusion protein and allowed to bind. After washing away unbound peptides, labeled bound material, representing the cellular or extracellular protein binding domain, can be eluted, purified, and analyzed for amino acid sequence. Peptides so identified can be produced synthetically or fused to appropriate facilitative proteins using recombinant DNA technology.

Example 11

Cell-Based Screening Assay for Agents that Decrease Viral Infection

This example describes methods using intact cells that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. For example, a yeast two-hybrid assay or the inverse two-hybrid assay method of Schreiber and coworkers (*Proc. Natl. Acad. Sci., USA* 94:13396, 1977) is used to screen for an agent that disrupts the association between a host protein (such as those listed in Table 1, proteins encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, and any target sequence associated with SEQ ID NOS: 229, 230, and 232) and a viral protein (such as HIV, Ebola, or influenza A virus). Similar to Example 10, therapeutic agents identified by these approaches are tested for their ability to decrease or inhibit infection of a host cell, such as a human cell, by HIV, Ebola, or influenza A.

In one example, the yeast two-hybrid system is used to identify anti-viral agents. One version of this system has been described (Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, 88:9578-82,

1991) and is commercially available from Clontech (Palo Alto, CA). Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one includes the DNA-binding domain of a transcription activator protein fused to one test protein "X" and the other includes the activator protein's activation domain fused to another test protein "Y". Thus, either "X" or "Y" in this system
5 can be a host protein (such as those listed in Table 1 and any target sequences associated with SEQ ID NOS: 1-232), while the other can be a test protein or peptide. The plasmids are transformed into a strain of *Saccharomyces cerevisiae* that contains a reporter gene (such as lacZ) whose regulatory region contains the activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid because it does not provide activation function
10 and the activation domain hybrid because it cannot localize to the activator's binding sites. Interaction of the two proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a host protein involved in viral infection. Total genomic or
15 cDNA sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of the host protein involved in viral infection fused to the DNA-binding domain are cotransformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. These colonies are purified and the plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the
20 library plasmids.

For example, and not by way of limitation, a host gene encoding a protein involved in viral infection (such as those listed in Table 1 and target sequences associated with SEQ ID NOS: 1-232) can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. A cDNA library of the cell line from which proteins that interact with
25 the host protein are to be detected can be made using methods routinely practiced in the art. In this particular system, the cDNA fragments can be inserted into a vector such that they are translationally fused to the activation domain of GAL4. This library can be co-transformed along with the host-GAL4 DNA binding domain fusion plasmid into a yeast strain which contains a lacZ gene driven by a promoter which contains GAL4 activation sequences. A cDNA encoded protein, fused to GAL4
30 activation domain, that interacts with the host protein will reconstitute an active GAL4 protein and thereby drive expression of the lacZ gene. Colonies which express lacZ can be detected by their blue color in the presence of X-gal. The cDNA can then be extracted from strains derived from these and used to produce and isolate the host protein-interacting protein using techniques routinely practiced in the art.

35

Example 12

Rapid Screening Assays

Prior to performing any assays to detect interference with the association of a host protein involved in viral infection and a viral protein such as an HIV, Ebola, or influenza A protein, rapid

screening assays can be used to screen a large number of agents to determine if they bind to the host or viral protein. Rapid screening assays for detecting binding to HIV proteins have been disclosed, for example in U.S. Patent No. 5,230,998, which is incorporated by reference. In that assay, a host protein (such as those listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or a viral protein, such as an HIV protein, is incubated with a first antibody capable of binding to the host or viral protein, and the agent to be screened. Excess unbound first antibody is washed and removed, and antibody bound to the host or viral protein is detected by adding a second labeled antibody which binds the first antibody. Excess unbound second antibody is then removed, and the amount of the label is quantitated. The effect of the binding effect is then determined in percentages by the formula: (quantity of the label in the absence of the test agent) - (quantity of the label in the presence of the test agent / quantity of the label in the absence of the test agent) x 100.

Agents that are found to have a high binding affinity to the host or viral protein can then be used in other assays more specifically designed to test inhibition of the host protein/viral protein interaction, or inhibition of viral replication.

15

Example 13

Assays for Measuring Inhibition of Viral Infection

Any of the test agents identified in the foregoing assay systems can be tested for their ability to decrease or inhibit infection by a pathogen or virus such as HIV, Ebola, or influenza A.

20

Cell-based assays

Exemplary methods are provided in Example 3 above. Briefly, cells (20,000 to 250,000) are infected with the desired pathogen, such as HIV, Ebola, or influenza A, and the incubation continued for 3-7 days. The test agent can be applied to the cells before, during, or after infection with the virus. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered, to identify optimal dose ranges. Following transfection, assays are conducted to determine the resistance of the cells to infection by various agents.

For example, the presence of a viral antigen can be determined by using antibody specific for the viral protein then detecting the antibody. In one example, the antibody that specifically binds to the viral protein is labeled, for example with a detectable marker such as a fluorephore. In another example, the antibody is detected by using a secondary antibody containing a label. The presence of bound antibody is then detected, for example using microscopy, flow cytometry, and ELISA.

Alternatively or in addition, the ability of the cells to survive viral infection is determined, for example by performing a cell viability assay, such as trypan blue exclusion.

35

Animal model assays

The ability of an agent, such as those identified using the methods provide above, to prevent or decrease infection by a virus, such as HIV, Ebola, or influenza A, can be assessed in animal

models. Several animal models for viral infection are known in the art. For example, mouse HIV models are disclosed in Sutton *et al.* (*Res. Initiat Treat. Action*, 8:22-4, 2003) and Pincus *et al.* (*AIDS Res. Hum. Retroviruses* 19:901-8, 2003); guinea pig models for Ebola infection are disclosed in Parren *et al.* (*J. Virol.* 76:6408-12, 2002) and Xu *et al.* (*Nat. Med.* 4:37-42, 1998); and cynomolgus monkey (*Macaca fascicularis*) models for influenza infection are disclosed in Kuiken *et al.* (*Vet. Pathol.* 40:304-10, 2003). Such animal models can also be used to test agents for an ability to ameliorate symptoms associated with viral infection. In addition, such animal models can be used to determine the LD50 and the ED50 in animal subjects, and such data can be used to determine the *in vivo* efficacy of potential agents.

10 Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, such as baboons, monkeys, and chimpanzees, can be used to generate an animal model of viral infection if needed.

15 The appropriate animal is inoculated with the desired virus, in the presence or absence of the test agents identified in the examples above. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered to different test subjects, to identify optimal dose ranges. The therapeutic agent can be administered before, during, or after infection with the virus. Subsequent to the treatment, animals are observed for the development of the appropriate viral infection and symptoms associated therewith. A decrease in the development of the appropriate viral infection, or
20 symptoms associated therewith, in the presence of the test agent provides evidence that the test agent is a therapeutic agent that can be used to decrease or even inhibit viral infection in a subject.

25 Having illustrated and described the principles of the invention by several examples, it should be apparent that those embodiments can be modified in arrangement and detail without departing from the principles of the invention. Thus, the invention includes all such embodiments and variations thereof, and their equivalents.

We claim:

1. A method of decreasing infection of a host cell by a virus, comprising interfering with an activity or expression of one or more host proteins or interfering with an activity of one or more host nucleic acids, wherein the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β -chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4; v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (LOC57826); LOC161005; osteoblast specific factor 2; Canis familiaris T-cell leukemia translocation-associated protein; aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2, testin 3; protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; similar to ribosomal protein L24-like (LOC149360); polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2); MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1 (ITGB1); acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule-like 1 (DSCAML1); LOC148529; Huntingtin-associated protein interacting protein (HAPIP); LOC158525

and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and hypothetical protein MGC14793; FLJ10439; cytochrome
 5 P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase (AXL), and wherein interfering with the activity or expression of the one or more host proteins
 10 decreases infection of the host cell by the virus.

2. The method of claim 1, wherein the one or more host proteins is encoded by one or more host nucleic acids comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

15

3. The method of claim 2, wherein the one or more host nucleic acids comprises any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

4. The method of claim 1, wherein the method comprises interfering with an activity or
 20 expression of more than one of the host proteins.

5. The method of claim 1, wherein the method comprises interfering with an activity or expression of at least three of the host proteins.

25 6. The method of claim 1 wherein the virus is HIV-1 or HIV-2, and the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β -chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III; LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-
 30 stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins; RAP-2A (LOC57826); LOC161005; Rab9, or osteoblast specific factor 2.

35 7. The method of claim 6, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

8. The method of claim 6, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

9. The method of claim 1 wherein the virus is influenza A, and the host protein is a *Canis familiaris* T-cell leukemia translocation-associated protein, aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between
 5 LOC253121 and hyaluronan synthase 2; testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; Rab9, or a myeloid/lymphoma or mixed lineage leukemia, translocated to 10.
10. The method of claim 9, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.
11. The method of claim 9, wherein the method comprises interfering with expression of
 15 one or more of the host nucleic acids.
12. The method of claim 1 wherein the virus is Ebola, and the host protein is a exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C; alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9
 20 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine B, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase; MGC40489; Rab9; PRO1617; retinoblastoma binding
 25 protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [*Hydractinia echinata*] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4; including UPS9X; LOC221829; U3 small
 30 nuclear RNA; integrin, beta 1 (ITGB1); acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box
 35 polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HBP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); *Mus musculus* 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1 (DSCAML1); LOC148529;

Huntingtin-associated protein interacting protein (HAPIP); LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and
5 hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase.

10

13. The method of claim 12, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

14. The method of claim 12, wherein the method comprises interfering with expression of
15 one or more of the host nucleic acids.

15. The method of claim 6, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

20

16. The method of claim 6, wherein one or more host proteins is encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

25 17. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any of SEQ ID NOS: 36-63 or a coding sequence of any of SEQ ID NOS: 36-63.

30 18. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 36-63.

35 19. The method of claim 12, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

20. The method of claim 12, wherein one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

21. The method of claim 1, wherein interfering with the activity of the one or more host proteins comprises decreasing an interaction of a viral protein and the one or more host proteins by disrupting or decreasing expression of the one or more host proteins.

5

22. The method of claim 21, wherein the viral protein comprises a virus and decreasing the interaction of the viral protein and the one or more host proteins decreases or inhibits infection of a host cell by the virus.

10

23. The method of claim 21, wherein disrupting or decreasing expression of the host protein comprises disrupting or decreasing transcription of an mRNA encoding the host protein.

24. The method of claim 23, wherein disrupting or decreasing transcription of the mRNA comprises inserting a transposon or insertional vector into a coding region of the nucleic acid encoding the host protein.

15

25. The method of claim 23, wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, RNAi, ribozyme, or siRNA that recognizes the mRNA.

20

26. The method of claim 1 wherein interfering with the activity of the host protein comprises decreasing an interaction of a viral protein and the host protein by contacting the cell with an agent that decreases or inhibits the activity or expression of the host protein or that disrupts expression of the host protein.

25

27. The method of claim 26, wherein the host cell is present in a host subject and wherein contacting the cell with the agent comprises administering the agent to the subject.

28. The method of claim 1, wherein the host cell is a mammalian host cell.

30

29. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising, decreasing an interaction between a viral nucleic acid and a host nucleic acid by decreasing the integration of the viral nucleic acid into the host nucleic acid, wherein the host nucleic acid comprises at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

35

30. The method of claim 29, wherein the viral nucleic acid comprises a viral genome and the host nucleic acid comprises a host genome.

31. A method of treating an HIV, Ebola, or influenza A viral infection in a host subject, comprising administering to a subject having a viral infection an effective amount of an agent that interferes with the interaction of a virus and host protein, wherein the host protein is encoded by a nucleic acid comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-
5 227, 229, and 231.

32. The method of claim 31, wherein the agent disrupts expression of the nucleic acid encoding the host protein.

10 33. The method of claim 32, wherein the agent is an antisense, ribozyme, or siRNA molecule that recognizes the nucleic acid sequence comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

15 34. The method of claim 31, wherein the effective amount induces a prophylactic effect in the host, which inhibits infection of the host by a virus.

35. The method of claim 31, wherein the host was previously infected by a virus and the effective amount induces a therapeutic effect in the host.

20 36. A method of determining resistance or susceptibility to viral infection in a subject, comprising comparing a first nucleic acid sequence of a subject to a second nucleic acid sequence comprising any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, wherein a higher similarity between the first and second nucleic acid sequence indicates the subject is more susceptible to viral infection, and wherein a lesser similarity between the first and second nucleic acid sequence
25 indicates the subject is more resistant to viral infection.

37. The method of claim 36, wherein the first nucleic acid sequence is obtained from a biological sample of the subject.

30 38. The method of claim 37, wherein the first nucleic acid sequence comprises a plurality of nucleic acid sequences, wherein each nucleic acid sequence is obtained from a different subject.

39. The method according to claim 36, further comprising determining a polymorphic variation within a population.

35

40. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising: contacting the host cell with an anti-protein binding agent that selectively or specifically binds to a host protein encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231 or a protein sequence shown in any of SEQ ID NOS: 228, 230, or 232, wherein the anti-protein

binding agent inhibits an interaction between the host protein and the HIV, Ebola, or influenza A virus.

5 41. The method of claim 40, wherein the host cell is present in a subject, and contacting the host cell with the anti-protein binding agent comprises administering the anti-protein binding agent to the subject.

42. The method of claim 40, wherein the anti-protein binding agent is an antibody or chemical compound.

10

43. A method of identifying a compound that decreases binding of a viral protein to a host protein and decreases viral infection, comprising:

15 contacting the host protein with the viral protein and a test compound, wherein the host protein is a protein in Table 1, and the viral protein is an HIV, Ebola, or influenza A protein; and determining whether binding of the viral protein to the host protein is decreased in the presence of the test compound, the decrease in binding being an indication that the test compound decreases the binding of viral protein to the target protein, and decreases viral infection.

20 44. The method of claim 43, wherein the viral protein comprises a virus.

45. The method of claim 43, wherein the viral protein is a viral envelope protein.

46. The method of claim 43, wherein the viral protein is an HIV protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 1-35.

25

47. The method of 43, wherein the viral protein is an influenza A protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 36-63.

30 48. The method of claim 43, wherein the viral protein is an Ebola protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 64-227, 229, and 231.

49. The method of claim 43, wherein the method comprises expressing the host protein in a cell, and contacting the host protein with the viral protein and a test compound comprises exposing the cell to the viral protein and the test compound.

35

50. The method of claim 43, wherein the host protein or the viral protein comprises a label, and determining whether binding is decreased comprises detecting an amount of label present.

51. A method of decreasing infection of a host cell by a pathogen, comprising interfering with an activity or expression of a Rab9 in the host cell, wherein interfering with Rab9 activity or expression decreases infection of the host cell by the pathogen.

5 52. The method of claim 51, wherein the pathogen hijacks a lipid raft.

53. The method of claim 51, wherein the pathogen is a *Campylobacter jejuni*, *Vibrio cholerae*, SV40, *Legionella pneumophila*, *Aeromonas hydrophila*, Echovirus 1, Echovirus 11, *Brucella* spp, *Clostridium* spp., Avian sarcoma and leukosis virus, FimH, Dr *Escherichia coli*,
10 *Streptococcus pyogenes*, Semiliki forest virus, *Salmonella typhimurium*, *Bacillus anthracis*, Ecotropic mouse leukaemia virus, *Shigella flexneri*, *Bacillus thuringiensis*, HTLV-1, *Chlamydia* spp., *Helicobacter pylori*, HIV-1, *Mycobacterium* spp., *Lysteria monocytogenes*, *Ebola*, *Marburg*, Measles, Herpes Simplex virus, influenza virus, or Epstein-Barr virus.

15 54. The method of claim 51, wherein the Rab9 host protein is encoded by a host nucleic acid comprising at least 90% identity to a target sequence associated with any of SEQ ID NOS: 118-119.

20 55. The method of claim 54, wherein the host nucleic acid comprises a target sequence associated with any of SEQ ID NOS: 118-119.

56. The method of claim 51, wherein interfering with expression of Rab9 comprises disrupting or decreasing transcription of an mRNA encoding the Rab9 protein.

25 57. The method of claim 56 wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA.

30 58. The method of claim 57, wherein the siRNA sequence comprises any of SEQ ID NOS: 232-235.

59. The method of claim 57, wherein the host cell is present in a subject, and contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA comprises administering the antisense RNA, ribozyme, or siRNA to the subject.

35

60. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the cell has a decreased susceptibility to HIV infection.

61. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the cell has a decreased susceptibility to influenza infection.
- 5 62. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the cell has a decreased susceptibility to Ebola infection.
63. A cell comprising a functional deletion of a Rab9 gene, wherein the cell has a decreased susceptibility to infection by a pathogen that uses lipid rafts.
- 10 64. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the mammal has decreased susceptibility to infection by HIV.
- 15 65. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the mammal has decreased susceptibility to infection by influenza.
- 20 66. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the mammal has decreased susceptibility to infection by Ebola.
67. A non-human transgenic mammal comprising a functional deletion of a Rab9 gene, wherein the mammal has decreased susceptibility to infection by a pathogen that uses a lipid raft.
- 25 68. The method of claim 1, wherein interfering with an activity of the host nucleic acid comprising administering one or more of SEQ ID NOS: 246- 845 to the host cell.

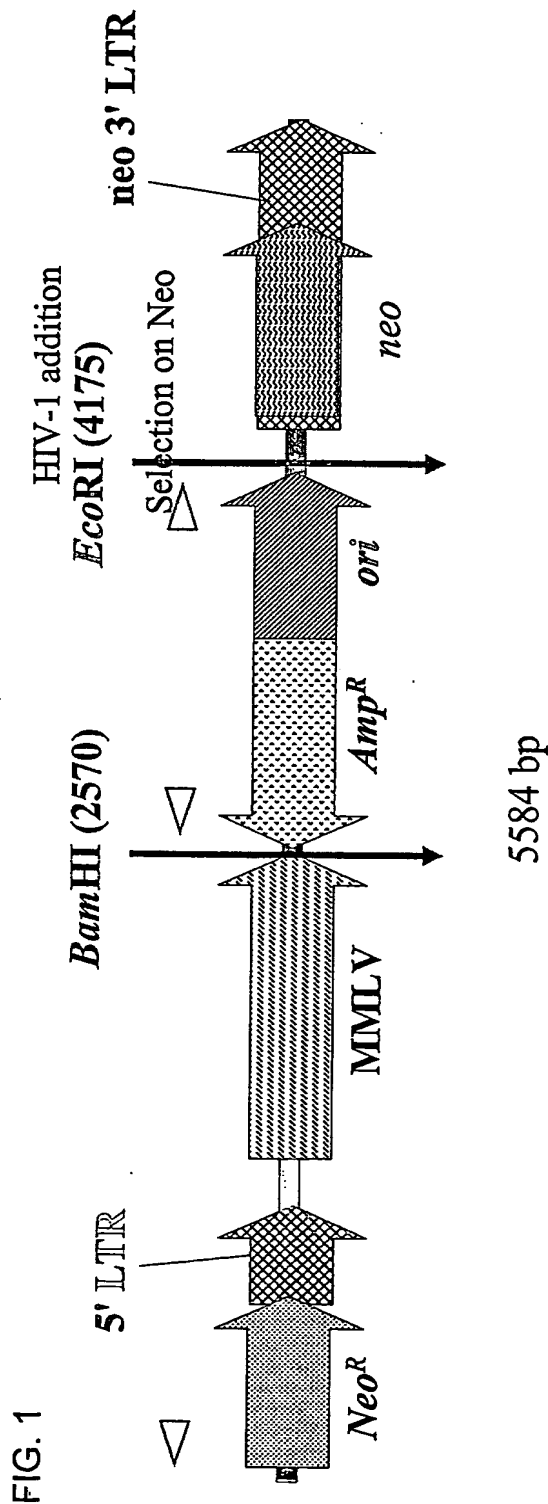
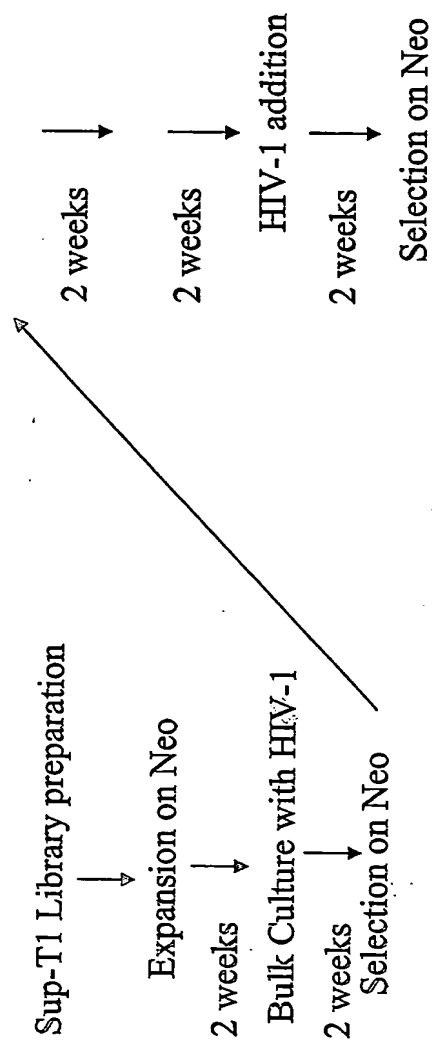


FIG.4



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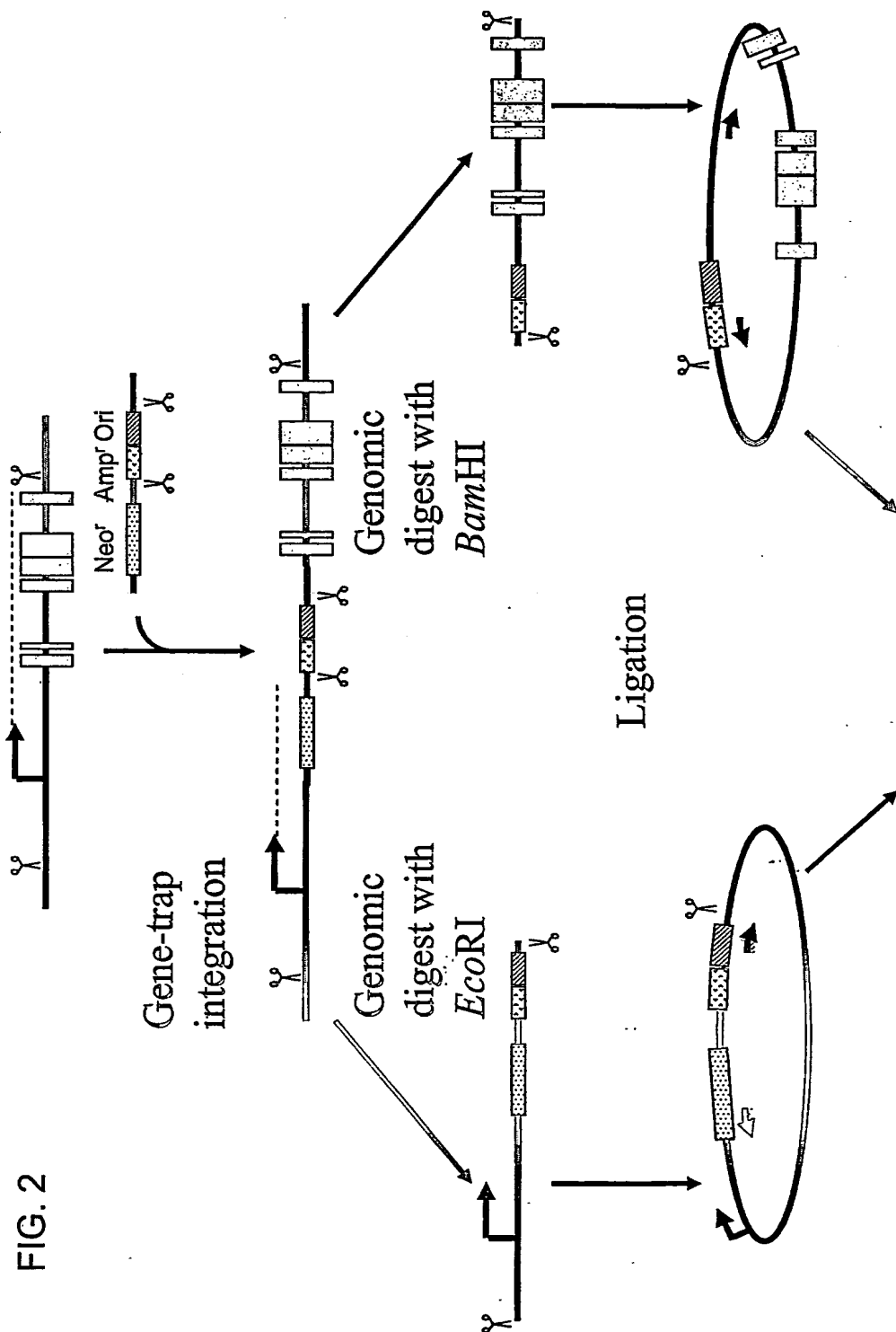
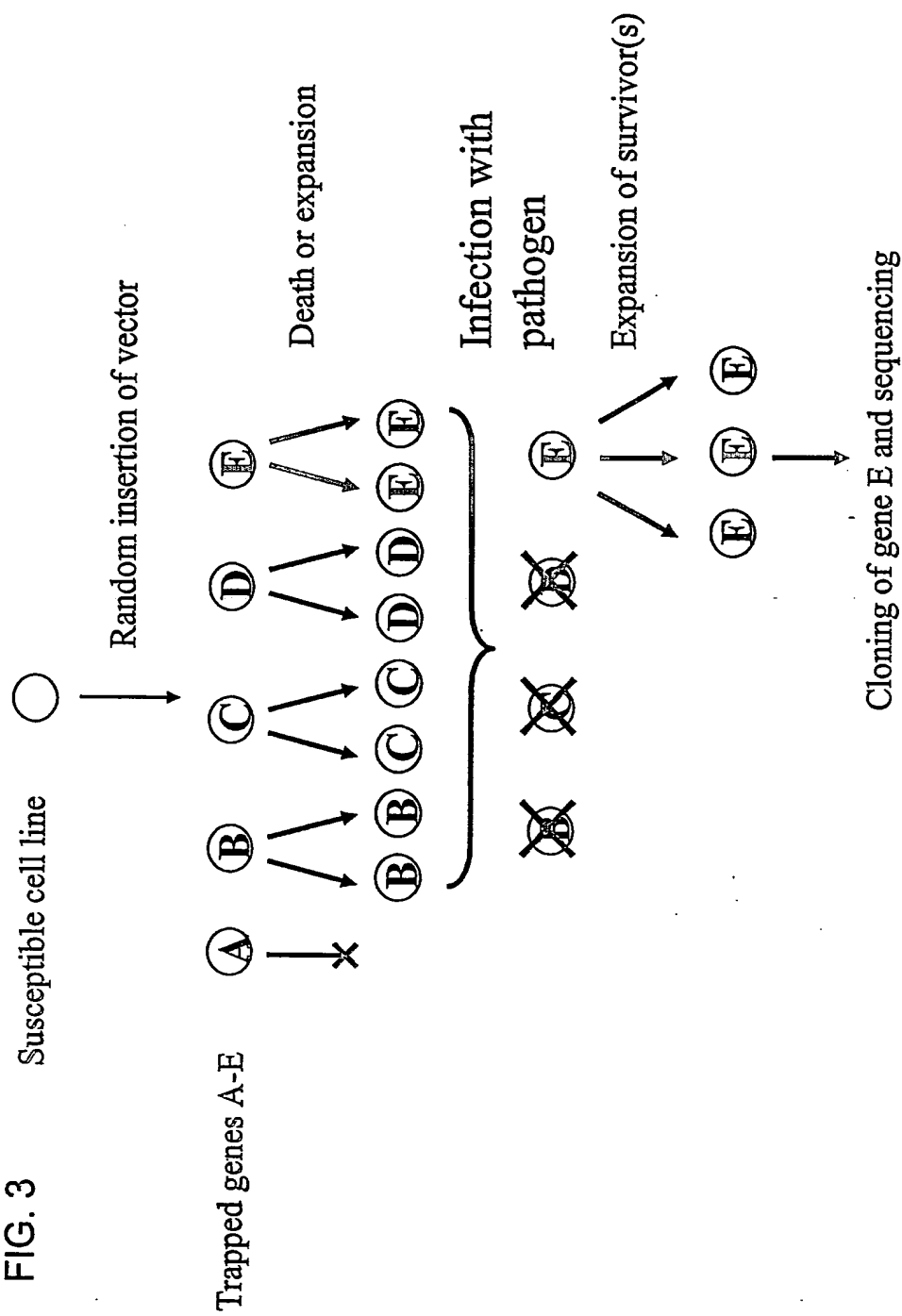


FIG. 2

Recover clones by transformation into bacteria and sequence

FIG. 3

Susceptible cell line



Trapped genes A-E

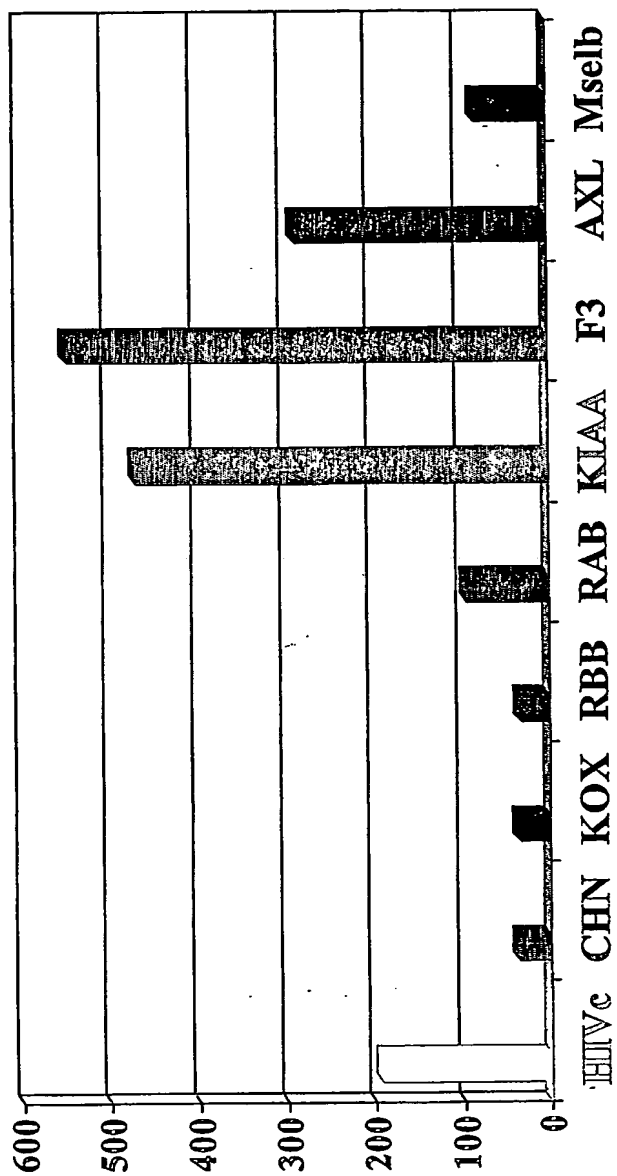
Death or expansion

Infection with pathogen

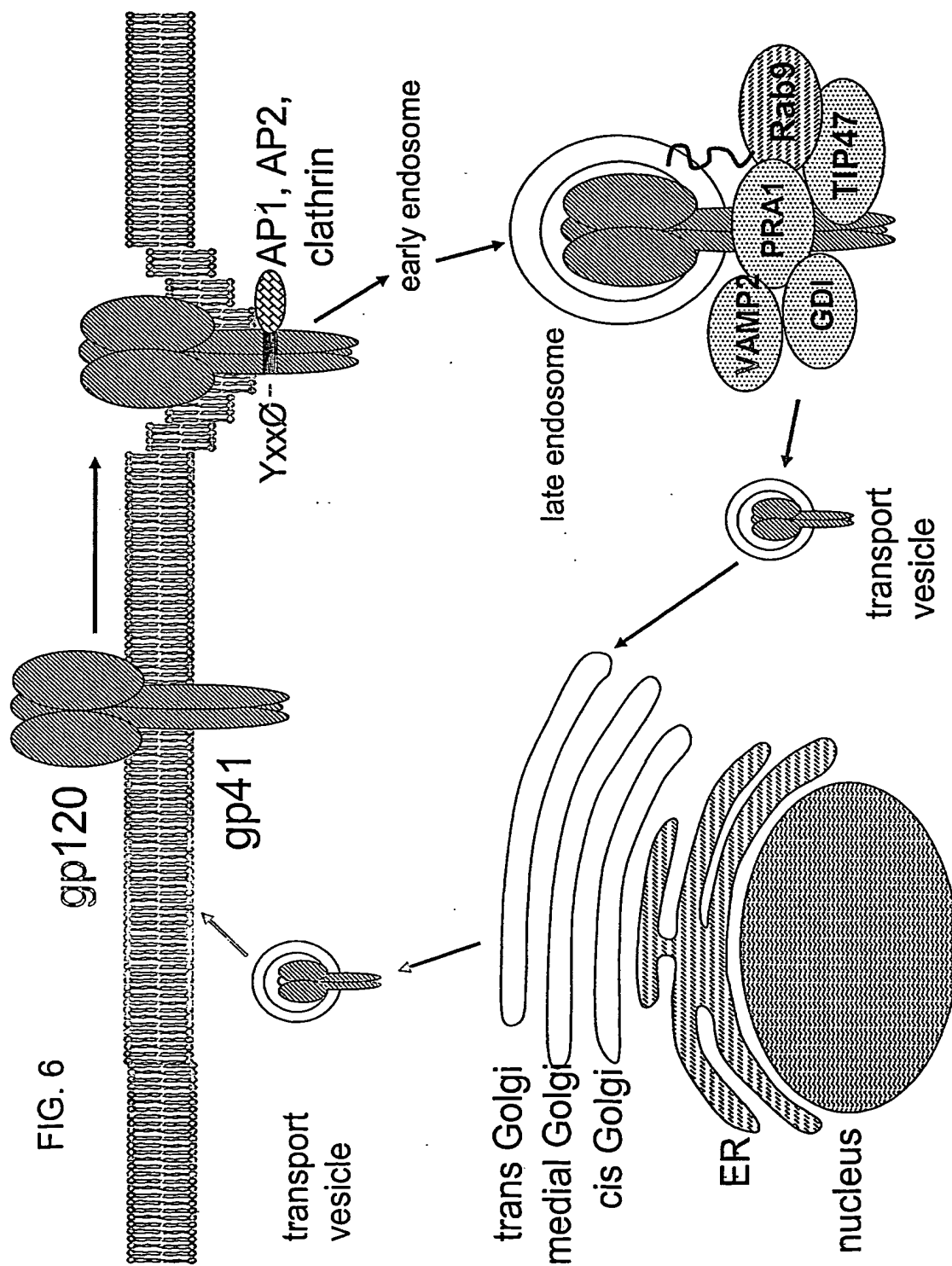
Expansion of survivor(s)

Cloning of gene E and sequencing

FIG. 5



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STATEMENT ACCOMPANYING SEQUENCE LISTING

The sequence listing does not include matter that goes beyond the disclosure in the international application.

The printout of the attached Sequence Listing is identical to the computer readable sequence listing on the enclosed computer disk.

SEQUENCE LISTING

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ctcggggcgc cagtcctccg attgactgag tcgcccgggt acccgtgtat ccaataaacc 420
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accagggcct ccagttctc attcagtatt ataatggaga agagagagca aaaggaaaca 600
ttcttgaacg attctccgca caacagttcc ctgacttgca ctctgaacta aacctgagct 660
ctctggagct gggggactca gctttgtatt tctgtgccag cagcgtaggt ggtagcttga 720
aacagttctt cggggcaggg acacggctca ccgtgctagg taagaagggg gctccagtgg 780
gagagagggt gagcagccca ncctgnncga ccccanancc tgttnttagg ggagtgnca 840
ctgggcatcc aggccctnct cnaggaancc ggttncccn ggnc 885

<210> 4
<211> 900
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(900)
<223> n is a, g, c, or t

<400> 4


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gaaaagcata cccacagtg tcagtggagg caacatgggg tcctggattt cctcttcacc      180
ctcagtggta gtgaggtgtt cctctcactc cttctgagta gaggaagcca agaggaaagc      240
tggaacttgt accatcatcc agtggtgata aagcctctgt ccctccacct tacccccagg      300
ttatcagtgg caaccacatg gctagtggta cccctcccgc tcctagccag aatgatatca      360
gcagaggcct agagagtagc ccaaaaactc atctgcaccc agcaggactg aggtttccta      420
ccccaccaa tggaagccaa gtgaggaacc taagccttca cctctcactc agcaggaacc      480
agacaacacc ccctaacaca cacacacaca cacacacaca cacacccttc tgttagtgtg      540
gtatcaagga ggcttgataa aatagaagat ttaaatagga tccattgccc ttatctcaaa      600
ctcttattat gaaatcactc ccttgagaga gaaaaaagcc tttttctctt ggattgtccc      660
agcagctccc gaccatcccc actcccacac cttatgtggc ccagcaatg agcctagtag      720
taggaaaatc tctatggata ctggtgctga tgggaagatt cttcctctca ngaagtgatg      780
gtgactgggg ctctgggatg ctcacgggaa tncatttcc cccacaagaa nttattttat      840
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```

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<210> 5
<211> 869
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(869)
<223> n is a, g, c, or t

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<400> 5
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ctactccatg ctaagttcag cgagaacttg gggtagccta gacattcttc cagagatgct      180
tttcttgtaa ctcttttcaa taagtaagca tgctttgctc tgcaactgggt gtcacctgtg      240
ttggatgctg ttgtccctgc cttgccctat attctgtcca catggtttct tcataggatg      300
atgcttaggt cagccctgag gtttgaacca gtcaacaagt ccaggttggg gtggagtccc      360
tttagtacct ccctttgcag gaataatgct gacccagaa actccctcag agcctctcca      420
ctggaggggc cttgtgacca ttcttggtt actcctcttg ttccagcatc ccatgtggcc      480
aatgggcccc ttctattttc aatggtatct caattcttac agtaagtgtat attattgccc      540
tacatcgaac tcatcttttc tcagtgttac ctgaggaaga atggagagga tgcccagaat      600

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tggcccagaa gaatccactt cgattctaga gaaaaaggca ggtagaggca gaagagattc 660
 acttcccagt gcatgcgtgc tgaatgttgg ggggtgttgtt tgagagagac aaggaaatgg 720
 ctgtaaaact tgggaagagg aacctgccct ggggtcaagta ggggtgttggg aggaccagat 780
 ggagcttgaa gctctctcca tctttgtcaa gtcccctgga ctgagagggn aaaatnacat 840
 ggcctttatc ctccagagga aantnattc 869

<210> 6
 <211> 850
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(850)
 <223> n is a, g, c, or t

<400> 6
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 gagttcttct gagcgggact ctgggggttcg aaatgagcta gcccttaagt aacgccattt 120
 tgcaaggcat ggaaaaatac ataactgaga atagaaaagt tcagatcgag gtcaggaaca 180
 gatggaacag ggtcgaccgg tcgaccggtc gaccctagag aaccatcaga tgtttccagg 240
 gtgccccaaag gacctgaaat gaccctgtgc cttatttgaa ctaaccaatc agttcgcttc 300
 tcgcttctgt tcgcgcgctt ctgctccccg agctcaataa aagagccac aaccctcac 360
 tcggggcgcc agtctccga ttgactgagt cgccgggta cccgtgtatc caataaacc 420
 tcttgacgtt gcatccgact tgtggtctcg ctgttccttg ggagggcttc ctctgagtga 480
 ttgactacc gtcagcgggg gtctttcact ctctgtgtac tggtagcaac agagcctgga 540
 ccagggcctc cagttcctca ttcagtatta taatggagaa gagagagcaa aaggaaacat 600
 tcttgaaaga ttctccgcac aacagttccc tgacttgac tctgaactaa acctgagctc 660
 tctggagctg ggggactcag ctttgtattt ctgtgccagc agcgtaggtg gtagcttgaa 720
 acagttcttc gggccaggga cacggctcac cgtgctaggt aagaaggggg ctccaggtgg 780
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 actgggncat 850

<210> 7
 <211> 847
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(847)
 <223> n is a, g, c, or t

<400> 7
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 gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg 120
 actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggacacagaag 180
 aaagcctcct gctgaagcca tcgttggccc acatgcattt cagggacaag aaatgaagat 240
 cggagacttt caagtgtgtc ccaggactca cctgctccca ggagacaaaa ggccacacag 300
 cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa 360
 gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc 420
 aacttgacat actttccctc gcaggccact ccagccact gtactctttg gcaggcctca 480
 ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag 540
 gactgaacac agtaccaaca taccacatc acaccttact ttcctctgcc cgccctgtcc 600
 ctgccctgac actgattccc cagcccttgc caccacagcc ccttcaccct ccactgcccg 660
 tgcagcagca gagacactcc ctccctgatg caaactgagg cctctggcac cccaactctt 720
 tcagggcaat gatagtctgt gcttaactct acatggccag gcccactca gggaattctc 780
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 tacagac 847

<210> 8
 <211> 755
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(755)
 <223> n is a, g, c, or t

<400> 8
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 taagtgaag tttattttta tttttttttt ttttttgaga cagagtctcg ctctgtcacc 120
 caggctagag tgcaaggcca tgatcttggc tcaactgcaac ctccacctcc caggttcaag 180
 tgattctctt gcctcagcct cccaagtagc tagtattaca gacgcctgcc accacgcccg 240
 gttaatTTTT gtacttttag tagagacagg ttccaccata ttggccaggc tggctcTaaa 300
 ctctgacct caggtgatcc tcctgcctca gcctcccaaa gtgctgggat tacaggcatg 360

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agctaccacg tctggcctaa gtgcatgtta cctatactaa caaaaccaca cttctgcctc 420
gaatgagaac agtctcctga acatcttgcc tctttgcctg actcaaagcc tcagggtctaa 480
gcctcccat aatttctagt ctcagcagaa agatcaatga caggagactc tccagggtgat 540
gaaattaacc aattaagtaa cctgggttgg catctcccg tttgttcacc agctcacctn 600
ctgccacagg tatatccttt ctctcancca tatatgcaca aacccctnc ccacggnaca 660
catannaana atttgaaga ctanaaaatc aggcanggtg tancncacct tnggggctgg 720
agtatggan cctgggccgg nacatncata cattg 755

<210> 9
<211> 839
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(839)
<223> n is a, g, c, or t

<400> 9
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accttacta caaggatatt acaacaggac attttttaaa acctcaaaca tcacaaaaat 120
ttctaagtgc aagtttattt ttattttttt ttttttttt gagacagagt ctgctctgt 180
caccagggt agagtgcagt ggcattgatc tggctcactg caacctccac ctccagggt 240
caagtgatc tcttgctca gcctcccaag tagctagtat tacagacgcc tgccaccacg 300
cccggttaat tttgtactt ttagtagaga caggtttcac catattggcc aggtgtgtc 360
caaactcctg acctcagggt atcctcctgc ctcagcctcc caaagtgtg ggattacagg 420
catgagctac cacgtctggc ctaagtgcatt gttacctata ctaacaaaac cacacttctg 480
cctcgaatga gaacagtctc ctgaacatct tgcctctttg cctgactcaa agcctcagg 540
ctaagcctcc ccataatttc tagtctcagc agaaagatca atgacaggag actctccagg 600
tgatgaaatt aaccaattaa gtaacctggg ttggcatcct cccgtttgtt caccagctca 660
cctctgcca caggatatc ctttctctca gccatatatg caciaacccc ctccccacgg 720
cacacataga aanaatttgg aagactagaa aatcaggcna gggnttanca caccttngag 780
ggctggagta tgganccng gnnccggan atncatncnn tngaaaactt gactatggg 839

<210> 10
<211> 829
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(829)
 <223> n is a, g, c, or t

<400> 10
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 ctagccctta agtaacgccca ttttgcaagg catggaaaaa tacataactg agaatagaaa 120
 agttcagatc gaggtcagga acagatggaa cagggtcgac cggtcgaccg gtcgacccta 180
 gagaaccatc agatgtttcc aggggtcccc aaggacctga aatgaccctg tgccttattt 240
 gaactaacca atcagttcgc ttctcgcttc tgttcgcgcg cttctgctcc ccgagctcaa 300
 taaaagagcc cacaaccct cactcggggc gccagtcctc cgattgactg agtcgcccgg 360
 gtaccctgtg atccaataaa ccctcttgca gttgcatccg acttgtggtc tcgctgttcc 420
 ttgggagggt ctccctctgag tgattgacta cccgtcagcg ggggtcttcc agtagccctt 480
 cctttgtagc aaagacagac agatgggtgat ccaagagata cgcaagaaga ggaccgtgtg 540
 tgtcatgggt gagctctaaa aaagagaaat cacttggatg gaantgaagg agaggaaaag 600
 gctgatgtgg atggcctgga agangttcga ttggttacct tggcaccgag cttccttcct 660
 catcctcatn cctccctagt ccttgttctt aaaaanantt ttctttctaa ngtccttcc 720
 ccctccncaa gggggcaciaa ggatntttaa aaaacncctt tccgggcnta attttaacct 780
 angatccatc ccagncctgt nccnnttttc nnagattcat ttaaacnng 829

<210> 11
 <211> 710
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(710)
 <223> n is a, g, c, or t

<400> 11
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 tgacgagttc ttctgagcgg gactctgggg ttcgaaatga gctagccctt aagtaacgcc 120
 attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg 180
 aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaacctat cagatgtttc 240
 cagggtgccc caaggacctg aaatgacctt gtgccttatt tgaactaacc aatcagttcg 300
 cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc 360
 tcactcgggg cgccagtcct ccgattgact gagtcgcccg ggtaccctgt tatccaataa 420

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accctcttgc agttgcatcc gacttgtggt ctcgctgttc cttgggaggg tctcctctga 480
gtgattgact acccgtcagc gggggctctt cagtagccct tcctttgtag caaagacaga 540
cagatgggtga tccaagagat acgcaagaag aggaccgtgt gtgtaatggt tgagctctaa 600
aaagagaaat cacttggatg gaaatgaagg agaggaaagg ctgatgtgga tggctgggaa 660
gagggttcgat gggtaccttg gcanccganc ttcnttntcn atncccatcc 710
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<210> 12
<211> 752
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(752)
<223> n is a, g, c, or t

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<400> 12
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aggcaactct ctcttccac ctgccccca aactccctc cacctccctc cacatgtatc 120
ctcccacttc cttccactca tgtaatgaga ggtgctgatg agtcacagga gaggtagccc 180
tagataacca acagactgca aaacggacag tccttggatg tctgagccag tgtttgtgca 240
ctgcattgac tggctcctcg tagtttttct ctgtagttgc taaagcctgt aaggtctgtg 300
tgatgaatat tttctaacac atcttagaag aacataatgc aagacagaat gaaaaactag 360
agaggcagaa acccccaaag taagtagtgg gaaattacca ggtatataat aggtcaagcc 420
tgctctgcag gagctcaagg gattgtagca ttcttatccc aaaccactga atcctgggca 480
aaaataagaa gtcgccta at ttagtatta ccagcttccc aaccccgggc attcttcac 540
ttactcaagc tgtccagagg ccccgagggt actccctata agtcccatgg gtggctgaga 600
tctatttaga ggcacaaggg tatctnctta taagtccaat gggngggctg agatetatga 660
gaagcatctt gggggagagt gccntttggc caccagcatg tggncctna attttncatg 720
nnncaactgg nccngggaag gaaaantttt ga 752
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<210> 13
<211> 749
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(749)
<223> n is a, g, c, or t

<400> 13

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cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgaggtcag      180
gaacagatgg aacagggtcg accggtcgac cggtcgaccc tagagaacca tcagatgttt      240
ccagggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc      300
gcttctcgct tctgttcgcg cgcttctgct ccccgagctc aataaaagag cccacaaccc      360
ctcactcggg gcgccagtc tccgattgac tgagtcgccc gggtagccgt gtatccaata      420
aaccctcttg cagttgcac cgacttctgg tctcgctgtt ccttgggagg gtctcctctg      480
agtgattgac taccgctcag cgggggtctt tcagtagccc ttcctttgta gcaaagacag      540
acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagcttta      600
aaaaangaga aatcacttgg atggaaatga agganaggaa aaggcntgat ntngatngcn      660
gggaaanagg ttccatnggt ncttttggnn anccgannct tnccttctcn atcccntnc      720
cntccctann nccntnnttn ttaaaaaag      749

```

<210> 14

<211> 794

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(794)

<223> n is a, g, c, or t

<400> 14

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cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgaggtcag      180
gaacagatgg aacagggtcg accggtcgac cggtcgaccc tagagaacca tcagatgttt      240
ccagggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc      300
gcttctcgct tctgttcgcg cgcttctgct ccccgagctc aataaaagag cccacaaccc      360
ctcactcggg gcgccagtc tccgattgac tgagtcgccc gggtagccgt gtatccaata      420
aaccctcttg cagttgcac cgacttctgg tctcgctgtt ccttgggagg gtctcctctg      480
agtgattgac taccgctcag cgggggtctt tcagtagccc ttcctttgta gcaaagacag      540
acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagctcta      600
aaaaagagaa atcacttgga tggaaatgaa ggagaggaaa aggctgatgt ggatggctgg      660

```

gaagagggttc gatggttacc ttggcaaccg agcttccttn ctcattccca tccctnecta 720
 gtccttggttc tttaaaaaga tttntttnt aatgtccctt nccctccaca agggggcaca 780
 agatgttttn aaac 794

<210> 15
 <211> 784
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(784)
 <223> n is a, g, c, or t

<400> 15
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 agttctcagg gngaacaaaa aattgtatgt gtgcagaacc tgtgatttgc ctgcacatag 120
 tcaagttctc aatgtatgga tgtcccgccc caggctacca tactccagcc ctcaaggtgt 180
 gctatacett gcctgatttt ctagtcttcc aaattcttct atgtgtgccg tggggagggg 240
 gtttgtgcat atatggctga gagaaaggat atacctgtgg caggaggtga gctggtgaac 300
 aaacggggagg atgccaaccc aggttactta attgggtaat ttcacaccc ggagagtctc 360
 ctgtcattga tctttctgct gagactagaa attatgggga ggcttagacc tgaggctttg 420
 agtcaggcaa agaggcaaga tggtcaggag actgtttctca ttcgaggcag aagtgtggtt 480
 ttgttagtat aggtaacatg cacttaggcc agacgtggta gctcatgcct gtaatcccag 540
 cactttggga ggctgaggca ggaggatcac ctgaggtcag gagttttgag accagcctgg 600
 ccaatatggg ggaacacctg tctctactaa aaagtacaaa aattaacccg gncgtngng 660
 gcaggnntc tgtaatacta nntacttgg gngntgnag gcaanaaaat cantttgaac 720
 ctnggnaggg gngngnttgc aatnnccna aaanatgcc cnntggncct ttaaccntgg 780
 gngn 784

<210> 16
 <211> 757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(757)
 <223> n is a, g, c, or t

<400> 16


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acatTTTTTTT aaacctcaaa catcaccaaaa atttctaagt gcaagtttat ttttattttt      120
TTTTTTTTTT ttttgagaca gagtctcgct ctgtcaccca ggctagagtg cagtggcatg      180
atcttggctc actgcaacct ccacctccca ggttcaagtg attctcttgc ctcagcctcc      240
caagtagcta gtattacaga cgcctgccac cagcccggt taatttttgt acttttagta      300
gagacagggt tcaccatatt ggccaggctg gtctcaaact cctgacctca ggtgatcctc      360
ctgcctcagc ctcccaaagt gctgggatta caggcatgag ctaccacgtc tggcctaagt      420
gcattgttacc tatactaaca aaaccacact tctgcctcga atgagaacag tctcctgaac      480
atcttgcctc tttgcctgac tcaaagcctc aggtctaagc ctcccataa tttctagtct      540

tggttggca tcctccggt tggtcaccag ctacactnct gncacaggta tatncttttt      660
tctnagccat atatgcccaa anccccctnc ccacgnaca catngaagaa ntnnggaaga      720
ctngaaaatc aggccagggt tngcccacc ttngggg      757

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```

<210> 17
<211> 783
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(783)
<223> n is a, g, c, or t

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<400> 17
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TTTTTTTTTT TTTTTTTTTT ttgagacaga gtctcgctct gtcacccagg ctagagtgca      180
gtggcatgat cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgcct      240
cagcctccca agtagctagt attacagacg cctgccacca cgcccggtta atttttgtac      300
ttttagtaga gacaggtttc accatattgg ccaggctggt ctcaaactcc tgacctcagg      360
tgatcctcct gcctcagcct cccaaagtgc tgggattaca ggcatgagct accacgtctg      420
gcctaagtgc atgttaccta tactaacaaa accacacttc tgcctcgaat gagaacagtc      480
tcctgaacat cttgcctctt tgctgactc aaagcctcag gtctaagcct ccccataatt      540
tctagtctca gcagaaagat caatgacagg agactctcca ggtgatgaaa ttaaccaatt      600
aagtaacctg ggttggcatc ctcccgtttg ttcaccagct cacctcctgc cacagggtata      660
tcctttctct cagccatata tgcacaaacc ccctnccac ggcacacata gaagaatttg      720

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gaagactaga aaatcaggca nggtatagca caccttggag ggctggagta tggtagcctg 780
ggc 783

<210> 18
<211> 770
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(770)
<223> n is a, g, c, or t

<400> 18
tccgggnncc gcttgccaaa ccttcagggtg gggctctttca ctacaagata gtacaacagg 60
acattttttta aaacctcaaa catcaccaaa atttctaagt gcaagtttat ttttattttt 120
tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtga gtggcatgat 180
cttggtctac tgcaacctcc acctcccagg ttcaagtgat tctcttgct cagcctccca 240
agtagctagt attacagacg cctgccacca cgcccggta atttttgtac ttttagtaga 300
gacaggtttc accatattgg ccaggctgggt ctcaaactcc tgacctcagg tgatcctcct 360
gcctcagcct cccaaagtgc tgggattaca ggcatgagct accacgtctg gcctaagtgc 420
atgttaccta tactaacaaa accacacttc tgctcgaat gagaacagtc tcctgaacat 480
cttgctcttt tgctgactc aaagcctcag gtctaagcct ccccataaatt tctagtctca 540
gcagaaagat caatgacagg agactctcca ggtgatgaaa ttaaccaatt aagtaacctg 600
ggttggcatc ctccgtttg ttcaccagct cacctnctgc cacaggtata tcctttttct 660
tagccatata tgcacaaacc cccttccac ggnacacata gaaaaatttn ggaagactag 720
aaaatcaggc aggtntagc acaccttngn gggctnggag tntnggtanc 770

<210> 19
<211> 774
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(774)
<223> n is a, g, c, or t

<400> 19
tccgggncnc gcttgccaaa ccttcagggtg gggctctttca ctacaagata gtacaacagg 60
acattttttta aaacctcaaa catcaccaaa atttctaagt gcaagtttat ttttattttt 120
tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtga gtggcatgat 180

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cttggtcac tgcaacctcc acctcccagg ttcaagtgat tctcttgct cagcctccca 240
agtagctagt attacagacg cctgccacca cgcccgggta atttttgtac ttttagtaga 300
gacagggttc accatattgg ccaggctggt ctcaaactcc tgacctcagg tgatcctcct 360
gcctcagcct cccaaagtgc tgggattaca ggcattgagct accacgtctg gcctaagtgc 420
atgttaccta tactaacaaa accacacttc tgcctcgaat gagaacagtc tcctgaacat 480
cttgctctct tgcctgactc aaagcctcag gtctaagcct ncccataatt tctagtctca 540
gcagaaagat caatgacagg agactctnca ggtgatgaaa ttaaccaatt aagtaacctg 600
ggttggcatc ctcccgtttg ntcaccagnc tnacctnctg ncacaggnat atnctttnt 660
ttnagccata tntgcacaaa cccctnccc acggnacaca tagaaaaant tnggnagact 720
ngaaaattca ggncagggnt tagcncnccc ttgggggnnt ggnntntngg aacc 774

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<210> 20
<211> 914
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(914)
<223> n is a, g, c, or t

```

```

<400> 20
tggggnntncc ggtatcgccg cttecgattc gcagcgcac gccttctatc gccttcttga 60
cgagttcttc tgagcgggac tctgggggtc gaaatgagct agcccttaag taacgccatt 120
ttgcaaggca tggaaaaata cataactgag aatagaaaag ttcagatcga ggtcaggaac 180
agatggaaca ggtcgaccg gtcgaccggt cgaccctaga gaaccatcag atgtttccag 240
ggtgccccaa ggacctgaaa tgacctgtg ccttatttga actaaccaat cagtctgctt 300
ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata aaagagccca caaccctca 360
ctcggggcgc cagtcctcgc attgactgag tgcgccgggt acccgtgtat ccaataaacc 420
ctcttgagct tgcattcgac ttgtggtctc gctgttcctt gggagggtct cctctgagtg 480
attgactacc cgtcagcggg ggtctttcac tctctgtgta ctggtaccaa cagagcctgg 540
accagggcct ccagttcctc attcagtatt ataatggaga agagagagca aaaggaaaca 600
ttcttgaacg atttccgca caacagttcc ctgacttgca ctctgaacta aacctgagct 660
ctctggagct gggggactca gcttttgtat ttctgtgcca gcagcgtagg tggtagcttg 720
aaacagttct tcngggccag gggacnccg tnaccgggnn aggtaagaag ggggcctcca 780
ggtgggaaan aagggtgagc agnccanccc tgcacgaccc nnaaccntn ttcttagggg 840

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gaggggnnca ctgggncatn ncagggccnt cntngnggaa nnggggtttg cgccnagggt 900
 ccccagggt gngc 914

<210> 21
 <211> 1604
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1604)
 <223> n is a, g, c, or t

<400> 21
 gngtggmatt gtgagcggat aacaatttca cacagnaatt cagtaaattgt tgatgtcaca 60
 ttgggggagcag cagctctagc tacattcaac tctacctgaa aactggcttt tagtataagc 120
 catggatcca taacacatag gctagtttac aacaagtaat ttcagcattt ttggataatt 180
 acattccctc cgacaatttc taaggagcct gcatgatact gaactgtgtc agaaaatagg 240
 tgctacagtg aatatgtgat tctaatacagg cttttttact atggaattat agtaaaatgc 300
 actataatca actcatataa attgctctgt gcctatactt atctctaattg aagggaagca 360
 aattgcctta cctgaaatta taaaagaaaa tgattacaaa ggtatggaag tttataggca 420
 tcttataaga cctgatttta ttatgcatta tatagatggc aaaaaattcc tatttatcca 480
 gaatctaaat gaccaggaag ctcaaataaa atgtgtttca tgggaatttg tttttatgtg 540
 ctgaattgca agatcctgaa gggctcttaa gatcatcaaa gaaacatgaa tgctcacaca 600
 acttttagagc tgtaagaggt gtggagttca catggcccaa cctgtccatt tgacagctgc 660
 gtgctgagcc caggggagag catggcttgc ccaatgaatt tgtgacaaag cgagacctgg 720
 rgnnaccttt cagtttcctt yataccccac aaatgggtct ttgtgctcta ctaggkgnaa 780
 tggattataa taccacagnc cttttgtgta ttctaantyc ttagaaattt cctaatttat 840
 gcatgggycc mccccttgcta aaatttcagc atacaccatg atatcttaga gctcccttcc 900
 cacttaattc tctctcttag cattttcacg atttaaaaaa atcatctgta ttccccatta 960
 gcaggcaaga ttccctaagga caaataactt tttttctttt attcactgct gaatcaccta 1020
 gaacgggtacc cagcaciaag tgagaggttg agaaatagtt gttgaatgaa aaaaaaatg 1080
 aatcgtttat gataatcctc aaatcccac actgcattat cagaataccc cattttttat 1140
 gtcacttatt tgacactttt ccagaacttc tgatgtgcca ggcattttac aaggctgagg 1200
 tgaaccacag agtaataggc ttattttatt cattcagga gcttaattta aggtgatcct 1260
 attattgtaa cctcctaattg caatgtcatc tcttatcagc ttaattctgc agactgtagc 1320

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tatgtattac tccctgaagg aattatatttc accttcaacc tgaagttagg actcatgatt 1380
cagcaatctg ctttctggga tcatacaagg gaaattgcaa tctttgtgct tgcttgccaa 1440
agctgagaaa gatggagcag natcaaaata agcaggattt gccaggcaat tttgacatat 1500
tcttcctctc acatataacc atcacaaagt aatgcatttc ataatgagaa ganccttgca 1560
ctagaagcat acatagtatc acatgnctca tcttctngnt tctn 1604

<210> 22
<211> 844
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(844)
<223> n is a, g, c, or t

<400> 22
ttggggancc gcttgccaaa cnttcagggtg gggctcttca agaggctctcc agacctaggg 60
gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg 120
actccagaat ccactggggc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag 180
aaagcctcct gctgaagcca tcgttggccc acatgcattt cagggacaag aaatgaagat 240
cggagacttt caagtgtgct ccaggactca cctgctccca ggagacaaaa ggccacacag 300
cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa 360
gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc 420
acactgacat actttcccct gcaggccact ccagcccact gtactctttg gcaggcctca 480
ggttctgcta ctccatgtac tattcctgtc ttgcacagge cagaagctaa aggtgaggag 540

ctgccctgac actgattccc cagcccttgc accccagccc cttcaccctc cactgcccg 660
gcagcagcag agacactccc tccttgatgc aaactgagge ctctggcacc cnactctttc 720
agggcaatga tagtctgtgc ttaactctac atggccagge cccactcagg gaattcttat 780
gaaattatta ttttttnta tttctgggaa acaaagcgat gtatttattt ctgtttnggg 840
gata 844

<210> 23
<211> 1562
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(1562)

<223> n is a, g, c, or t

<400> 23

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ttttacanaa ctnnncccc tnaatcaaca gaatatacat tttnttnagc cccncaatac      60
acttatttcta aantgnccca cataatngga agtaaaccac tcagcaaata taaagancag      120
aaatcccanc aaactgtctc tcagaccaca gtgcaatcaa attagaactc agggttaaga      180
atcacactca aaaccacaca actacatgga aactgaacaa cctgctcctg aatgactact      240
gggtaaataa tgaaatgaag gcagaaataa acacgttctt tgaaaccaac tagaacaag      300
acacaatgta ccagaatctc tgggacacat ttaaagcagt gtgtagaggg aaatttatag      360
cactaaatgc ccacaagaga aagcaggaga gatctaaaat cgacatccta acatcacaa      420
taaaagaact agagaagcaa gagcaaacat attcaaaagc tagcagaaga cgagaaataa      480
ctaagatcag agcagaactg aaggagatag agacacaaaa aaaaccttca aaaattaatg      540
aatgcaggag ctggtttttt gaaaagatca acaaaatagc cctctagcaa gactaataaa      600
ggataaaaga gggagaatc aaatagatgc aataaaaatg ataaagggga tatcaccacc      660
aatcccmcmg aaatacaaac taccmtcaga gaatactata aacmcctgta tgcaataaaa      720
ctagaaaatc tagaagaagc agataaattc ctggacacat acaacctccc aagactaaac      780
caggaagaag ttgaatctct gaatagacca ataatagggt ctgaaattga ggcaataatt      840
aatagcctac caaccaaraa aagtcgagga ccagatggat tcacagccgt attctaccag      900
aggtacaaaag aggagctggt accattcctt ctgaaactat tctgatcaat gagaaaaaag      960
ggaatcctcc ctaactcatt tatgaggcta gcacatcctt gataccaaag cctggcagag     1020
acacaacaaa aaaagaaaat ttcaggccaa tatccctgat gaacattgat gtgaaaatcc     1080
tcaatacaat actggcaaat caaaaagctt atccaccacg atcaagtcag cttcatcgct     1140
gggatgcaag tctggttcaa catatgcaaa tcaataaaca aaatccatca cataaacaga     1200
accaatgaca aaaaccacat gattatctca atagatgcag aaaaggcctt caacaatatt     1260
caacagcctt tcatgctaaa aactctcaat aaactagata ttgatggaac atatctcaac     1320
ataataagag ctatttatga caaaccata gccaatatca tactgaatgg gcaaaaactg     1380
gaagcattcc ctttgaaaac cagcacaaga caaggatgcc ctctttcacc acttcgattc     1440
aacctagtat tggaagttct ggccagggcc atcaagcaag agaaagcaat aaggggtatt     1500
caagtaggaa gagaggggnt ttctgtgtga aaangttanc cgctggnnan ccccaaanan     1560
aa                                                                 1562

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<210> 24

<211> 1446

<212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1446)
 <223> n is a, g, c, or t

<400> 24
 ttggtactgt cagaccaagt ttactcatat cggatccgag gagcaggcgg gcctgaggcc 60
 gagtcagctg cgcgggcccc cggatcctgg gctgtcatgt aacatcttcc aataaatgtg 120
 atcttgggag gagaccattt tgggccttgg tttccacatc tgcgaaatgt tattatagcc 180
 atgaacactt actgaaagct taccocatat gccagacaca tcttccaatc aacttatgtg 240
 agttatctca ttaattttt acaacaatac aaagtagcgg ggaaaacttc tggcttctct 300
 tgaaaactca gaaaatctaa caatgttgag tatgagcca aaatgtcagc aagaagccag 360
 agctgaatag ggaaggctgt tttagatgag accattagcc acagacctca ccactcttct 420
 tactgtgcta cttatttctt ttatagtacc tgagtgttcc ctgtgcgtg tgggtttgtg 480
 gccctgcat tagatggnc cttatnatc ctcttcaccc ctgagctttg atgttttttg 540
 ctccatgtca ccttcaccag agtggtcagg ccattcttca atattcwkac ctrggcaaaa 600
 ggtgcatgac tttgaactcc cctagttaag ttaaggcttc takaawgaac angannangc 660
 tttgggagct gaggaagggg gctcactgtg ccctataaaa tagagtttca atagacactg 720
 ggtcctctgtt ggcctgacct cccctgtgtc agcaacttga gtctcacttg aatggggaaa 780
 gaaagtawtg arangaaakg aacwwkgaam ytcwgaaaca ngacctcttm akanswarcn 840
 aggrccctms tagctanyt wrggtaaagc caagtgtgac cctaaggcaa gttacttaac 900
 ctctgcgtct cagtttctc atctataagt taatgacaac ctctaccca taaggagct 960
 tgaaagaaaa tccaaaaaag aaagaatctc tttgagttgc taatgactct taagtttctg 1020
 gttctagtcc tttgaccatc atgacagtcc tatggtttta cgaaagaact atccatctct 1080
 atttaaaaaa caaaaaaac aaagaccttt tttgcttaag ctaacttgtg ttgggtttca 1140
 tccaccagga agttagagag agaaattact tagagataaa cttacacatt acaaatcctt 1200
 ctgttctgtg tgctttttaa aatgttcaat ttctaaatgg gcctctggtg aagataatga 1260
 tcacctcatt gatttgttcc caggagaaca gggtaaaatg aagtcctgct gatcacattt 1320
 tctaaatctt ttantccca ttgctttggg aaagtttcta caccagtnat ccttntacag 1380
 cctccctctt tcccatgggt cnttctctgc accaccagga aaggaggaat cccanancag 1440
 tcttgc 1446

<210> 25
 <211> 840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(840)
 <223> n is a, g, c, or t

<400> 25
 ggaattgna gcgntaaca atttcacaca gnaattctta ttatggtaag ttcctgagat 60
 ttgagatggt ttgttataca acaggggaact gataggctta ttcttcaaga ggagcaaaac 120
 agggatgatt gctattctct tcaatgggtt gaggaagaa gaaattatgt gaacatttat 180
 aactaataa tttattctgt catatttcag tcagattaaa gcaaacagcc aaaaacaagg 240
 acaaagtcca aggttaagaga ctgatgataa gtggcctgtt tacaaggaaa ataagatcac 300
 tagctctact tacagctgat tcagaataac ttcattttta aagcctaaaa ttttacagtc 360
 aagctcttga gtgcaatttc cttaacattt tctaaacct acagaaaatc ataaagaaac 420
 aatatttctt tgtttgagtt tccttttttag gagttaggtc ttatttttaa aatattttct 480
 agcctgttta ggctcttatt taaaattatc tacttttctc aaagtcttct tcatacttga 540
 gatatccaaa atattgaatg agtgatgtaa actataccag ataaactatg agtctatatt 600
 tttaccctga ttcagtcagt ttccaaggag aactttgaac aactaaaaat gtgtattact 660
 ataatctctc tgaaatattn ctnattaatt ttttgggggn aaaatgagtc attctgagcc 720
 aaaaaaaaa anggtnacca gacantttcc actnctaact tgnntgggcg attncagcag 780
 attcaanttc cagcatnggn agatncggna gatnnnggnc ctacatgan cttaccttcc 840

<210> 26
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(861)
 <223> n is a, g, c, or t

<400> 26
 ttttntctct aacttgagtt ggcatatca gcagattcaa attaccagca atgggaagat 60
 acaggaagat gtaggtacct accaatgagc ttacctccc agtgctctat ataacctcac 120
 ttctatagcc caaagtatta aaaagaagaa aaaataataa ttcaggctta ctatttaaaa 180
 atacagtgat tctggccggg cacggtggct cagcactgca atcccagcac tttgggaggc 240

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cgagggcgggt ggatcacgtg aggccaggag tttgagacca gcctggccaa tgtggtgaaa 300
ccctgtctcc actaaaaata caaaaattag ctgggcattg tggcgggcgc ctgtaatccc 360
agctactcgg gaggttgaga tgggagaatt gcttggaccc aggaggcaga gcttgcagtg 420
agccaagatt gcaccactgc attccaccct gggtgacaga gtgagaccct gtctcaaaaa 480
acaaataaaa atacagtgat tctgagaggg cttccctttc cacaccacct cctacttggt 540
tgatagctct catcccat tctcaactg ccacatatgg ccaggacttc cacagtgtat 600
taaacatctt ctttgacaa gagaaatttc actgaagcaa tgagtgtaga agttattagc 660
atgaattgaa gactgatgct ggcacacaaa tagggagaca catcaatata atgacctaat 720
gaatctagaa atagcttcan gaantntgga aaagtagatg tgataaaagn tgcatttnaa 780
tcannagaca aagtnttaat anaattgaga cacctatgtn gctattngga aacattaang 840
tnggntgcat antngaaact t 861

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<210> 27
<211> 875
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)..(875)
<223> n is a, g, c, or t

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```

<400> 27
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gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg 120
actccagaat ccaactgggc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag 180
aaagcctcct gctgaagcca tcgttggccc acatgcattt caggggacaag aaannnagat 240
cggagacttt caagttgtgc ccaggactca cctgctocca ggagacaaaa ggccacacag 300
cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa 360
gcattctgaa gttcctaage tcccttcttc ctgataggag cattgacctg tgatgtcacc 420
aactgacat actttccct gcaggccact ccagccact gtactctttg gcaggcctca 480
ggttctgcta ctccatgtac tattctgtc ttgcacaggg cagaagctaa aggtgaggag 540
gactgaacac agtaccaaca taccacatc acaccttact ttcctctgcc cgccctgtcc 600
ctgccctgac actgattccc cagcccttgc caccacagcc ccttcacct ccactgcccg 660
tgcagcagca gagacactcc ctctttagtg caaactgagg cctctggcac cccaactctt 720
tcagggcaat gatagtctgt gcttaactct acatggccag gccccactc agggaattct 780

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aatatgaatg taaactncag gtgttgncag ctagtgcttc cntggaaaan cccctgttnc 840
 agctnctaca catgctctta tctntagctn ganca 875

<210> 28
 <211> 901
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(901)
 <223> n is a, g, c, or t

<400> 28
 ctncctctng gngtntnnnn nacnatntan nnnnatcgc tcnacantnn nttncnnggg 60
 aaaaacctct gtctaacctt acatgaaaaa acccgtttcc aacgaaggcc tctaagaggg 120
 caagatatcc acttgagac tttacaaaca gagggtttcc aaactgctga atgaaaagaa 180
 aagttaaact ctgtgagttg aacgcacaca tcacagagca gtttctgaga atgattctgt 240
 cgggttttta tacgaagata ttcccttttc tgcctttggc ctcaaagcgc ttgaagtctc 300
 cacttgcaaa ttgcagaaaa agagtgttcc gaactctgctc tgtctaaaag aaggttcaac 360
 tctgtcagtt gaatacacac aacacaagga agttactgag atttcttctg tctagcctta 420
 catgaaaaaa acccgtttcc aacgaaggcc tcaaagaggt caaaatatcc acgtgcagac 480
 tttccaaaca gagggtttcc aaactgctga atgaaaagaa aagttaaact ctgtgagttg 540
 aacgcacaca tcccagagca gtttctgaga aagattctgt ctagttttta taggaaaata 600
 tttccttttc tgcctttggc ctcaaagtgc ttgaaatctc cacttgcaaa ttccacaaaa 660
 agagtgttcc aaactctgctc tgtctaaagg aaggttgaac tctgtgagtt gcatacacac 720
 aacacaaaga agttactgag aaatcttctg tctagcataa tatgaagaaa tcccgtttcc 780
 acgaaggcct caagaggnc aatatncaact ggcaggcttn caacagagtg ttntactgctc 840
 tctgtgaaag aangntaact ttgnngttga ccaccatnan aagnnttttg naanatttgn 900
 n 901

<210> 29
 <211> 856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(856)
 <223> n is a, g, c, or t

<400> 29
 cnttttggnng tttaaaangg gcnganatat gcttnacatc nattgggggn aaacctcttg 60
 cgtgagtatt caagaacctt ctcttgggat ctggatcggg acccctttcc tgtaacatat 120
 gcaaggaaag aatgcagag gaatggaact gagccatgga acagacattt ggggttgggc 180
 aggaggagtt agcagagaga tctgcatagc tcttataccta cttagcacta gtgctgttca 240
 aggtagaact cacagcataa gaattctagc atctgcataa atttgagag caacttgcct 300
 tctccttaga tacacgaata tggaaaatgc aatagaagtt gcttatcatg cactcagggt 360
 gagtgaagtt ttatcataat gaagctaaat gaaattccca aattgctctg gtggagagga 420
 acgccttgat attccacttg tggaaaaatg gctctatgcc aaaaataaag ttacatcaac 480
 ctcatgacag gagaaatcag agtttctgct cacagcagca gcagaggaat catctgcaac 540
 acagagactt ttgggttgta tgtaaggcag ccttgctgga tggctcttaa cagggttttg 600
 gtagggacat ggtagaggct ggctcctaaa ctcttcaaac gtttcttccc agccctttag 660
 ctttgacctc acgtgcagag ttgagttaat tataagcctt atttatgggc acactttcac 720
 cattaagtgc atacacagcc ccatttttgc gccattcttc actcctatgt cttttctccc 780
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 tcatttacac atgatt 856

<210> 30
 <211> 890
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(890)
 <223> n is a, g, c, or t

<400> 30
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 aaaaancccca gnactccata attcncaagn atcacatgna tcacaggaga ggagactggg 120
 ggagtcaatg gatagaggat ttataagcca agaaaaaaaa atggagcccc aaactgtgaa 180
 atccaagaag ggggtcatgt gaaccccaat ttatagccag tttttcagaa gaataagtga 240
 caacctacta cttgtgattg gcacttgaag tgggaggcag tcgtgaggga gttaatatgt 300
 gggaactaac cctactctag gtagtggtga attgaatcaa atcataggac atctagtgtg 360
 tgtttgctgg aaaactgggt gttggtggag tgaaaccctt acatattttg gtgatcagag 420
 gtgaagtgtt gtgttaagtg gtatgagact gggaaaaaca ctttggtttt tcctgtctct 480
 cacagaatta aagtttccaa gagaagcatc agaagagtgg aagggttgga ccagcaaacc 540

```

acaagcccta ggccccaac tagggtcaag tggaaaagca gggataata gtgaaatggc      600
cctcctctcc acttctgcag ctccagtgc gctgttcccta ctcatgtca cactggaatg      660
gttgaggat gaacacgac ctctggaaat ggagacatct tctgaaggta gaggaactg      720
cagtcttctt gccccgacc gccactcgca gaggttggga atgtcagcct nctccaacct      780
antcttttnt atgggatttt ccttactttg gggggggact gnaatgntac ctatcttttt      840
tttacaantt gggggggntc cnccccactt anngaccng nttnnccng      890

```

```

<210> 31
<211> 732
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(732)
<223> n is a, g, c, or t

```

```

<400> 31
attcttttgg gnaccgtcag naccaagttt tactcatatc ggcatcctct ctgggtggct      60
gctgcagcgg ggctgggtgt ctgcaaccg gacggagctg agtgaggggc acaatggcag      120
caacctgcag gcaccaaaga gcccccaaga gctgctcagc ggtgcctgat caaagtttgt      180
ctgggccagt gcttgtgcat tgtgtacgct gtgcgacaac caggaaggag agctgggttt      240
tgccatcctc caacgcttct taaataggaa actttttggg tagcacctgg cctagttcct      300
ggaacacaga aggtgctgag tgatgttagt ttcattcgt catcttgtct cttgggcatg      360
gaaaagagtt tacaagtgt ctttcattat ccatcttgat gtgggaaggt ggggcagggg      420
aagatgagta cccgctctcg ccctttgggt tgatgtttgt gacgtacatg aggcagtgtg      480
gagagtggat cacagcattg gacagactgg atcccttctg gtcccacatc actcaggcaa      540
ctctctcttc ccacctgccc cccaaactcc cttncacctc cctccacatg tatcctccca      600
cttncttcca ctcatgtaat gagaggtgct gatgagtcac aggaagaggt agccctagat      660
aaccaacaga ctgcaaacg ggacagtncc ntggatgtct gagccagtgt ttngngcact      720
gcattgactg gc      732

```

```

<210> 32
<211> 672
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

<222> (1)..(672)

<223> n is a, g, c, or t

<400> 32

```

tttggnaacc gtcagaccaa gtttactcat atcggatccc aggagacacg ctccaagggc      60
tgggtgggaa aagccccaga aaggggaggg ctgcggggag tgagaatcgg gatggacctc      120
acagacgaca aacagatgga caaaaagctt ctctccctgc cgctccctcc ccgccaccaa      180
ctccagcccc tctgtctcca tccccctttc ctgtctgtcc tgtctgaatc tctgaatctc      240
tgcctgtttt tttttctctc tatgaatcac agcgtttcag agcctctgag agaaaaatgg      300
gaaaagaaga cagagatgat agaaaatgca gagtgtgcgt gtgtgtgtgt gtgtgtgcat      360
gtgtatgccc gcgtgtgtgt gtgtgtctgt gcatgcgtgc acccagcatg aagtctggtc      420
tggagaatgt aactaggagg ggaggaagag aggggacgag agaagcagag gatgaacaaa      480
gagacttttc aagctcatag gaaaaagcct gggaggcaac agcagcaggg acacgcatat      540
gccgcacacc cctacacaca ccacacacca cacaccacac acaccctgca tgcaccctgg      600
agacatgccc cagactccag gcgggagggg tggagcaggg ggtgtgaaat atggttggtt      660
gggttgggtt tg                                     672

```

<210> 33

<211> 770

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(770)

<223> n is a, g, c, or t

<400> 33

```

nttttgnant gtncgcggn tacaatttca cacagnaatt cattttaacg ttgtacatat      60
ttattatata agaaatattt tttccatcaa aaagtactca ttcaaaaaat atttaattcta      120
gaatagagat tataaatttt taacttaatt ttattttttt cttaaggaaa actctaagat      180
atcattacca ttttcaaaac tgtcaagtag tggatgaatga cacttcttat atgttaattt      240
ttaaaagaat atttctaaca cacattctta atggagaatt atatcttata cagaatgata      300
cattctaagg gtgatgttta tgaagaaat ttaagcttgg ttaacatgct tagtaaaatt      360
ttttaatata aataaaattc agagtatatg gtgtgaagtg agttatatgg tgcaaaatact      420
attttaattc ttgaacactt ccacaaaatt agcttgtaaa ataaaattaa acccactg      480
agatgctaga tttgcagatg aatcattcat ttttttacat ttctttttat ttctctaact      540
aaattatatg acagaaggca agggatcatg ttaattcatt gttgtattct ttatatatta      600

```

aatataagct cctcaataaa tattatggaa aaaatgaaca aacacttcac attttattgt 660
 tttctatatatt tttcaagggt tttattaatt cttcatgtgc tttgtgactt tattttctcc 720
 aaagaaattc ttcttgaaat gaaaagttca caanagttag gataactgga 770

<210> 34
 <211> 777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(777)
 <223> n is a, g, c, or t

<400> 34
 nttnnatt gtngcgcggn taacaatttt cacacagnaa ttcttttgtc aagaattata 60
 agaagaaatc cgttttccaa cgaaggcctc aaagagttcc aaatatccac ttgcacactg 120
 cacaactaa gtctttccaa actgctctat gcaaagaaat gttcaactct gtgagtttaa 180
 tacacacatc acaaagcagt ttctgagaat gatactgtct agtttttata cgaagatatt 240
 tccttttgta ccattggcct catactgcta gaattttcca cttgcaaatt ccacaaaaag 300
 agtgtttcca atccgctctg tctaaaggaa ggttcaactc tctgatttga atacatacat 360
 caatataaaa cgtagattgt cacttcaaga aaatacctgc cttatacaga actaagtggc 480
 tgtttcaagt aaaaatgggt ttccatgaaa aagctgctag ttcagctggc aactcaaaca 540
 atggcacaag tgccttatgc catttctatt ttatcacaca tattaataaac ctggccagca 600
 cgggtggtca tgcctgtaat tccagcattt tggnaaggcc gaggcagggt gatcatttga 660
 ggccagnagt tcaagacang cctggccaac atagcaaac cccattttt actaaaatac 720
 aaaattagcc aggcntgggg gcgcgtgcct gtantccnnc ttctcgggag gctgagg 777

<210> 35
 <211> 799
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(799)
 <223> n is a, g, c, or t

<400> 35
 tnnttttga gtgancgagg ntaacaattt tacacaggaa ttctagggtt ggttcatggt 60
 ttgagacttg agagtggaca ggtgcctagt tagacctgct ctggatgtgg aggtgtctgg 120

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tgattagaat gactctttgt atatctgttc cctctttaat tgcttccttt taacctcaag 180
attaggcttt tattgcataa taaaatgcat atgagccatt cagttttact ccattacctc 240
tctggccttag aatgaactat cagtagaatt aacaaaaatt gcatcataga gttggagaat 300
tgccaccaag gaagtgttct agccatacta cagaaaagat tctcccatg ggattacttc 360
tcagtagaat tcagcaacca attcctggtg aatctatcca agcagagaaa tgaaaacata 420
tattcactaa aagacttgaa cacaaatgct catagcagcc ttaatcaaaa tagagaaaaa 480
ctggaaacat ttcaaagtgc tatcaactga tcaatatata agcaaaatat ataaagcatt 540
tgcagacaat aaaaaacaaa atattgatat atactaaaac atggnatgaa cctcaaagcc 600
actatactag atgagagatg tcagacacaa acctactgta tttgcaagat gccatttact 660
tgaaaaatcc agaaaagtcg catttacaga gacagtaaaa cagataagtg ggctgcctgc 720
ggctgggggg ttgnaaaagc nattttgctg caaatgaact tanggaaatt ttttttgnng 780
ggggggngat anaaaattn 799

<210> 36
<211> 417
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(417)
<223> n is a, g, c, or t

<400> 36
ancttggttaa ctgtcagnac caagattttac tcatatcgga tccccaggaa tactattctt 60
taaagactat caatattcta caaagggaat ttagagttct caattgtgaa cggaaggaa 120
catcaatggg catgacctaa gacctccttc tacacagtta aacaacaatt tcacaagata 180
tgatttaaga gaaagcttcc agggacgcct ggggtggctca gtggttgagc gtctgccttc 240
cgctcagggt gtgatcctgg agttccggga ctgagtcctc atggggctcc ctgcatggag 300
cctgcttctc cctctgccta tgtctctgcc tctctctgtg tctcatgaat aaataaataa 360
agnncttatt ttttttaaga ttntatttat ttatnctga nagagagaga gaggcng 417

<210> 37
<211> 434
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(434)

<223> n is a, g, c, or t

<400> 37

```

tggtaactcg tcagnaccaa gatttactca tatcggcac cccaggaata ctattcttta      60
aagactatca atattctaca aagggaaatt agagttctca attgtgaacg gaaaggaaca      120
tcaatgggca tgacctaaga cctccttcta cacagttaaa caacaatttc acaagatatg      180
atttaagaga aagctttcag ggacgcctgg gtggctcagt gggtgagcgt ctgccttccg      240
ctcaggggtgt gatcctggag ttccgggact gagtcccaca tggggctccc tgcatggagc      300
ctgcttctcc ctctgcctat gtctctgcct ctctctgtgt ctcatgaata aataaataaa      360
gtccttattt tttttaagat tttatttatt tattcatgag agagagagag agncngngnc      420
ntnggcngng ggng                                         434

```

<210> 38

<211> 1425

<212> DNA

<213> Canis familiaris

<220>

<221> misc_feature

<222> (1)..(1425)

<223> n is a, g, c, or t

<400> 38

```

cnggncggng angattntng tcgnnaccca tggcgaatgc ctggctngcc gaatattcat      60
ggtggaaaat ggcngcttt tctggattca tcgnactgtg nccggctggg tgtggcggac      120
ccgctatnca gnacatagcg ttgggctacc cngtgataat gctgaagagc ttggcggncg      180
aatgggctga ccgcttctc gtgskkkanc ggtatcgccg ctcyccgatt cgcagcgcac      240
cgccttctat cgccttcttg acgagttctt ctgagcggga ctntctgggt tcgaaatgag      300
ctagccctta agtaacgcca ttttgcaagg catggaaaaa tacataactg agaatagaaa      360
agttcatctc tgctgtcttt ggccattctc tctaggcatc tgctcatgtg gaggcataag      420
aaaatattga catgcttcac attacatttt cagagtatgt tattcatgta atttatttgt      480
aaaatctacc aatacaattt cccccaatc aagtaaaact aggtaaaaag atctctgcaa      540
agattagctg aggaagaaac atatgtgagt agaatcagaa tgtaagagc tgacaggtta      600
gcagatagca tgcccatgat ttttgtgggt ttggccctt tgttgaagct aaatcttaca      660
gagaggccca accctagagg taaaatgatt aaaacagatg tgctgcagtt ggcggggagg      720
gtgctgcgcc aggggaagcc caagactgct gctggctgcc ttccctctg aycttatecc      780
atgtctcatt tgaaaaccaa tagttgaaaa actctcaatt ttcagatgag aacgaaaaca      840
aaaatgcaaa gaaggcaaat gattcaytca aarwtactca gtgaatkrga sccawsatgt      900

```



```

gggāataacaa ctctggcctt ctgtttctga atctagtggg atttccaggc teacaggaag      960
cttctctgtac cttgctccac tgtgtgtggt tttggatggc cctgggtgtt gattacctyt      1020
cgtggcaggc ccaacagccc ttgctaaggc acagactgca tatttgctga tccctgaggn      1080
ggaaagctgt gattcagact ttgaggtcta agaattgcag acttagtttc tagtctcccg      1140
atgaaactgc taatctgggt gccagtgggt tttctgtctac acggacacct gcccacacag      1200
catgattaga aattataatg atgacggcga tgagtcttcc aggacaccta cgttctttgc      1260
aagatatttc tgctaactgt ctctaccaga atcagttgga gaactttttt tagttttttt      1320
tttttttttt taatttcccc ctttctaagt caagtaaaaa tactagttta attnctgggt      1380
tagggtaatg atttgtcttc accattactg atgtgtcatt ttttg                        1425

```

```

<210> 39
<211> 674
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(674)
<223> n is a, g, c, or t

```

```

<400> 39
caaaaaatga cacatcagta atgggtgagga caaatcatta ccctacacca gnaattaaac      60
tagtattttt acttgactta gaaaggggga aattaaacaa aaaaaaaaaa aactaaaaaa      120
agttctccaa ctgattctgg tagagacgat tagcagaaat atcttgcaaa gaacgtaggt      180
gtcctggaag actcatcgcc gtcattatta taatttctaa tcatgctgtg tgggcagggt      240
tccgtgtagc agaaacacca ctggcaccca gattagcagt ttcacggga gactagaaac      300
taagtctgca attcttagac ctcaaagtct gaatcacagc tttccctca gggatcagca      360
aatatgcagt ctgtgcctta gcaagggctg ttgggcctgc cacgagaggt aatcaaacac      420
cagggccatc caaaaacaca cacagtggag caaggtacag gaagcttctt gtgagcctgg      480
aaataccact agattcagaa acagaaggcc agagttgtat tcccacatga tggctctaatt      540
tactgagta actttgaatg aatcatttgc cttctttgca tttttgtttt cgttctcatc      600
tgaaaattga gagtttttca actattgggt ttcaaagtag acatgggata agatcaggag      660
ggaaggcagc cagc                                                                674

```

```

<210> 40
<211> 666
<212> DNA
<213> Canis familiaris

```

<220>
 <221> misc_feature
 <222> (1)..(666)
 <223> n is a, g, c, or t

<400> 40
 cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccagn 60
 aattaaacta gtatTTTTTtac ttgacttaga aagggggaaa ttaaaaaaaaaa aaaaaaaaaa 120
 ctaaaaaaag ttctccaact gattctggta gagacgatta gcagaaatat cttgcaaaga 180
 acgtagggtgt cctggaagac tcatcgccgt catcattata atttctaatac atgctgtgtg 240
 ggcagggtgtc cgtgtagcag aaacaccact ggcacccaga ttagcagttt catcgggaga 300
 ctagaaacta agtctgcaat tcttagacct caaagtctga atcacagctt tcccctcagg 360
 gatcagcaaa tatgcagtct gtgccttagc aagggtctgtt ggcctgccca cgagaggtaa 420
 tcaaacacca gggccatcca aaaacacaca cagtggagca aggtacagga agcttcctgt 480
 gagcctggaa ataccactag attcagaaac agaaggccag agttgtattc ccacatgatg 540
 gctctaattc actgagtaac tttgaatgaa tcatttgcct tctttgcatt tttgttttcg 600
 ttctcatctg aaaattgaga gtttttcaac tattggtttt caaatgagac atgggataag 660
 atcagg 666

<210> 41
 <211> 603
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(603)
 <223> n is a, g, c, or t

<400> 41
 cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccaga 60
 attaaactag tatTTTTtact tgacttagaa aggggggaaat taaaaaaaaa aaaaaaaaaa 120
 taaaaaaagt tctccaactg attctggtag agacgattag cagaaatatc ttgcaaagaa 180
 cgtaggtgtc ctggaagact catcgccgtc atcattataa tttctaatac tgctgtgtgg 240
 gcagggtgtc gtgtagcaga aacaccactg gcaccagat tagcagttt atcgggagac 300
 tagaaactaa gtctgcaatt cttagacctc aaagtctgaa tcacagctt cccctcaggg 360
 atcagcaaat atgcagtctg tgccttagca agggctgttg ggcctgccac gagaggtaat 420
 caaacaccag ggccatcaa aaacacacac agtggagcaa ggtacaggaa gcttcctgtg 480

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agcctggaaa taccactaga ttcagaaaca gaaggccaga gttgtattcc cacatgatgg 540
ctctaattca ctgagtaact ttgaatgaat catttgcctt ctttgcattt ttgttttcgt 600
tct 603

<210> 42
<211> 749
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(749)
<223> n is a, g, c, or t

<400> 42
ggtactgtn cgnaccagtt tactncatat ncggnntccc atgagcaaaa aatgacacat 60
cagtaatggt gaggacaaat cattacccta caccagnaat taaactagta tttttacttg 120
acttagaaag ggggaaatta aaaaaaaaaa aaaaaaacta aaaaaagttc tccaactgat 180
tctggtagag acgattagca gaaatatctt gcaaagaacg taggtgtcct ggaagactca 240
tcgccgtcat cattataatt tctaatacatg ctgtgtgggc aggtgtccgt gtagcagaaa 300
caccactggc acccagatta gcagtttcat cgggagacta gaaactaagt ctgcaattct 360
tagacctcaa agtctgaatc acagctttcc cctcagggat cagcaaatat gcagtctgtg 420
ccttagcaag ggctgttggg cctgccacga gaggtaatca aacaccaggg ccatccaaaa 480
acacacacag tggagcaagg tacaggaagc ttcctgtgag cctggaaata ccactagatt 540
cagaaacaga aggccagagt tgtattccca catgatggct ctaattcact gagtaacttt 600
gaatgaatca tttgccttct ttgcattttt gttttcgttc tcatctgaaa attgagagtt 660
tttcaactat tggttttcaa atgagacatg ggataagatc aggaggggaag gcagccagca 720
gcagtcttgg gcttcccctg gcgcagcac 749

<210> 43
<211> 1778
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(1778)
<223> n is a, g, c, or t

<400> 43
gkggtagn gnrcggtaaaca atttncacac agcaattncc cctgtgnaaa ctgccttgac 60
ttggtgcctt ttttggaggg gtggagttgt ttccactttg acaaattttt atattttctcc 120

```

catcctaatt ggaetaattt gcttttatat ctcttctgtg gttattttgt taatcgtatt 180
ttaggaaagt cacctatttc aaattgattt gcatggagct aaataatttc ttccaatttt 240
ttcatttcct ttgtgtttat gggtatttct acattattag tgaaagtttt gtggttttgt 300
gttttagttc tctatctcct cttttgatta gtttcacaga gtttagttgt tattttttca 360
gaaaacagct cttgcactta tttatcggct ctactgttct taatttgctc ctaaaaattg 420
tcaataatat gtttcttttg ctttgcccg gctcattttg ttgtttttct aattgtttga 480
gcttgactct taattcatct atttttgttt ctgctttttt gttaatgtaa atttaaaaaa 540
tgcgagatcc aattagaata agcctcaccg gacaagaacc tgtctgtgca cttcgagact 600
accataatgc ctatcacata gcagggtgctt aagcaaaatt tttgtatgaa taaataaacc 660
cctatgaaat aattatggga tttgtgtgac agccctcggt cttctctgct gtctttggsc 720
aytctctcta ggcactctgt catgtggagg cataagaaaa tattgacatg cttcacatta 780
cattttcaga gtatgttatt catgtattta tttgtaaaat ctaccaatac aatttcccc 840
caatcaagta aaactaggta aaaagatctc tgcaaagatt agctgaggaa gaaacatatg 900
tgagtaraat caraatgtta agagctrmca gggtarcaga tagcatgcc atgatttttg 960
tgggkttggc ccctttgttg aagctaaatc ttacagagag gccaaccct agaggtaaaa 1020
tgattaaaac agatgtgctg cagttggcgg ggagggtgct gcgccarggg aagncccaag 1080
actgctgctg gctgccttcc ctccntgatc ttatcccatg tctcatttga aaaccaatag 1140
ttgaaaaact ctcaattttc agatgagaac gaaaacaaaa atgcaaagaa ggcaaatgat 1200
tcattcaaag ttactcagtg aattagagcc atcatgtggg aatacaactc tggccttctg 1260
tttctgaatc tagtgggtatt tccaggctca caggaagctt cctgtacctt gctccactgt 1320
gtgtgttttt ggatggccct ggtgtttgat tacctctcgt ggcaggccca acagcccttg 1380
ctaaggcaca gactgcatat ttgctgatcc ctgaggggaa agctgtgatt cagactttga 1440
gggtctaagaa ttgcagactt agtttctagt ctcccgatga aactgctaata ctgggtgcca 1500
gtgggtgtttc tgctacacgg acacctgccc acacagcatg attagaaatt ataataatga 1560
cggcgatgag tcttcagra cacctacgtt ctttgcaaga watttctgct aatcgnttnc 1620
tctaccagaa tcagtggag aacttttttt agtttttttt tttttttttt aatttcccc 1680
tttctaagtc aagtaaaaat actagtttaa ttctggtgta gggtaaatgat ttgtcctcac 1740
cattacttga aagacccac ctgtaggttg gcaagcgg 1778

```

<210> 44
 <211> 868
 <212> DNA

<213> Canis familiaris

<220>

<221> misc_feature

<222> (1)..(868)

<223> n is a, g, c, or t

<400> 44

```

ttcctgagac ngcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat      60
cattacccta caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa      120
aaaaaaaaaa aaaaaactaa aaaaagttct ccaactgatt ctggtagaga cgattagcag      180
aaatatcttg caaagaacgt aggtgtcctg gaagactcat cgccgtcatc attataattt      240
ctaactcatgc tgtgtgggca ggtgtccgtg tagcagaaac accactggca ccagattag      300
cagtttcatc gggagactag aaactaagtc tgcaattctt agacctcaa gtctgaatca      360
cagctttccc ctcagggatc agcaaatatg cagtctgtgc cttagcaagg gctgttgggc      420
ctgccacgag aggtaatcaa acaccagggc catccaaaaa cacacacagt ggagcaaggt      480
acaggaagct tcctgtgagc ctggaaatac cactagattc agaaacagaa ggccagagtt      540
gtattcccac atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt      600
tgcatttttg ttttctgtct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa      660
tgagacatgg gataagatca ggaggggaagg cagccagcag cagtcttggg cttccctggc      720
gcagcaccnt cccgccaaact gcagcacatc tgtttaatca tttaacctct aggntgggcc      780
tttctgtaag atttagcttn acaangggcc aaacccaaaa aatcatgggc atgcttctgc      840
tacctgncan tntaacattt gattntac                                          868

```

<210> 45

<211> 1237

<212> DNA

<213> Canis familiaris

<220>

<221> misc_feature

<222> (1)..(1237)

<223> n is a, g, c, or t

<400> 45

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gggatcgccg ctcccgattc gcaccgcac gccttctatc gccttcttga cgagttcttc      60
tgagcgggac tctgggggtc gaaatgagct agcccttaag taacgccatt ttgcaaggca      120
tggaaaaata cataactgag aatagaaaag ttcattctctg ctgtcttttg ccattctctc      180
taggcattctg ctcatgtgga ggcataagaa aatattgaca tgcttcacat tacattttca      240
gagtatgtta ttcattgtatt tatttgtaaa atctaccaat acaatttccc cccaatcaag      300

```

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taaaactagg taaaagatc tctgcaaga ttagctgagg aagaaacata tgtgagttaga 360
atcagaatgt taagagctga caggtagca gatagcatgc ccatgatttt tgtgggtttg 420
gcccctttgt tgaagctaaa tcttacagag aggcccaacc ctagaggtaa aatgattaaa 480
acagatgtgc tgcagttggc ggggaggggtg ctgcgccagg ggaagcccaa gactgctgct 540
ggctgccttc cctcctgac ttatccccat gtctcatttg aaaaaccaat agttgaaaaa 600
ctctcaattt tcagatgaga acgaaaacaa aaatgcaaag aaggcaaagt attcattcaa 660
agttactcag tgaattagag ccatcatgtg ggaatacaac tctggccttc tgtttctgaa 720
tctagtggta tttccaggct cacaggaagc ttctgtacc ttgctccact gtgtgtgttt 780
ttggatggcc ctggtgtttg attacctctc gtggcaggcc caacagccct tgctaaggca 840
cagactgcat atttgctgat ccctgagggg aaagctgtga ttcagacttt gaggtctaag 900
aattgcagac ttagtttcta gtctcccgat gaaactgcta atctgggtgc cagtgggtgt 960
tctgctacac ggacacctgc ccacacagca tgattagaaa ttataatgat gacggcgatg 1020
agtcttcag gacacctacg ttctttgcaa gatatttctg ctaatcgtct ctaccagaat 1080
cagttggaga acttttttta gttttttttt ttttttttta atttccccct ttctaagtca 1140
agtaaaaata ctagtttaat tctggtgtag ggtaatgatt tgtcctcacc attactgatg 1200
tgtcattttt tgctcatggg atccgatatg agtaaac 1237

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<211> 703
<212> DNA
<213> Canis familiaris

```

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<220>
<221> misc_feature
<222> (1)..(703)
<223> n is a, g, c, or t

```

```

<400> 46
ccctgtgaaa ctgccttgac ttggtgcctt ttttggaggg gtggagtgtt ttccactttg 60
acaaattttt atatttctcc catcctaatt ggactaattt gcttttatat ctcttctgtg 120
gttattttgt taatcgtatt ttaggaaagt cacctatttc aaattgattt gcatggagct 180
aaataatttc ttccaatttt ttcatttctt ttgtgtttat ggttatttct acattattag 240
tgaaagtttt gtggtttttg gtttttagttc tctatctcct cttttgatta gtttcacaga 300
gtttagtgtt tattttttca gaaaacagct ctgacactta tttatcggct ctactgttct 360
taatttgctc ctaaaaattg tcaataatat gtttcttttg ctttgcccg gctcattttg 420
ttgtttttct aattgtttga gcttgactct taattcatct atttttgttt ctgctttttt 480

```

gttaatgtaa atttaaaaaa tgcgagatcc aattagaata agcctcaccg gacaagaacc 540
 tgtctgtgca cttcgagact accataatgc ctatcacata gcaggtgctt aagcaaaatt 600
 tttgtatgaa taaataaacc cctatgaaaa aattatggga tttgtgtgac agccctcggt 660
 cttctctgct gncctttggcc attctctcta ggcactctgct cat 703

<210> 47
 <211> 304
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(304)
 <223> n is a, g, c, or t

<400> 47
 ctagcttgcc aaacctacag gtggggtctt tcaagtaatg gtgaggacaa atcattaccc 60
 tacaccagaa ttaaactagt atttttactt gacttagaaa gggggaaatt aaaaaaaaaa 120
 aaaaaaaact aaaaaagtt ctccaactga ttctggtaga gacgattagc agaaatatct 180
 tgcaaagaac gtaggtgtcc tggaagactc atcgccgtca tcattataat ttctaatacat 240
 gctgtgtggg caggtgtccg tgtagcagaa acaccactgg nccccagat nagagttttc 300
 ttgg 304

<210> 48
 <211> 735
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(735)
 <223> n is a, g, c, or t

<400> 48
 agcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat cattacccta 60
 caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa aaaaaaaaaa 120
 aaaaaactaa aaaaagttct ccaactgatt ctggtagaga cgattagcag aaatatcttg 180
 caaagaacgt aggtgtcctg gaagactcat cgccgtcatc attataattt ctaatcatgc 240
 tgtgtgggca ggtgtccgtg tagcagaaac accactggca cccagattag cagtttcatc 300
 gggagactag aaactaagtc tgcaattctt agacctcaaa gtctgaatca cagctttccc 360
 ctcagggatc agcaaatatg cagtctgtgc cttagcaagg gctgttgggc ctgccacgag 420
 aggtaatcaa acaccagggc catccaaaaa cacacacagt ggagcaagggt acaggaagct 480

tcctgtgagc ctggaaatac cactagattc agaaacagaa ggccagagtt gtattcccac 540
 atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt tgcatttttg 600
 ttttcgttct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa tgagacatgg 660
 gataagatca ggaggggaagg cagccagcag cagtcttggg ctttccctgg cgcaaaaccn 720
 tccccgcaac tggag 735

<210> 49
 <211> 1412
 <212> DNA
 <213> *Canis familiaris*

<220>
 <221> misc_feature
 <222> (1)..(1412)
 <223> n is a, g, c, or t

<400> 49
 cttcccacct nnnacccntg gnccttaaca gncacnnnc tttggagata gctaactcct 60
 acncattcaa catcagtgnn anggntctcc tccagaaggc ttcctcnacc ctttcaattc 120
 ccacttacnt gtaagcctag gatgcctcct ctcagattca gactggttgn cncagtgttt 180
 aagaacttna gctgtacagc canagagttt gtattggaaa ataactctctg tggttttttg 240
 tcnecatgat cttggacgag ttatttaacc ccctcagtnt agtttcttca tccatataat 300
 ctggcaaatg atagtncnca gtccatacaa ttgtnagcac taaacaaaat aatgtacacg 360
 agcctggcac actgaaggan ccagtgaaa ggtggttggtg attactnaca gtccttctca 420
 ttctctagca tagcacttac cgtgttgctg tccgatttct tgtctgcatg tctacctgca 480
 tgtcggtttg catgcagact atgaactgga agctgaatcc ccagtgcctg gtacaatgtg 540
 agaccccata ncagttcatt gaatgaattc agacacttca gtttttccat aaatttcagc 600
 cttcttcaat attttgcctc tattttctag aagtttctga aagagcagct tggaatatgt 660
 cagcaatttc taattttctta gcttttcagt gtgtgtgcgc gtgtgtgcgt gtgtgtttga 720
 tattttctgc tgtggaaacc gctggactta gatgatcagn ctgtgagata caggcaggac 780
 anagataaga agtaggagga gggctncgat gatgaagctt aggactgaa gcaactcagc 840
 caccaccag gaagcctcag tnccctgaar aggtggaccc tkkcasscyg wggatgaacca 900
 ttgtgggcca aagaggccca gtgcatgcat gaggcagacc tccctctaca gggaggcttt 960
 gccctactgg gatttatttc cttgctgctt aaggacctgg ctttgctcct gcctttcctt 1020
 gtcccttca tctgattctc tggccttatt ttggccagca gattgcaatt gcctgtccag 1080
 ttaccatat aaatgcattc tcctcctcat gacctcttct cagcctgctg gtctaaggga 1140


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ggagctctgt ttcttgatcc tgccctctga ctaaattttc tcttgctgct cttccctttc 1200
ctgatgattc agtacagaca cctgccaat tccacttttt ctcttcatct ccaattattt 1260
ggtggtcaag actgtttact caaatatgca tctggtttta tcacgagcca cgactctgac 1320
taaagtagcc tgattatatg gttctttaag ggatagctga ctttcacaaa cctaagaaaa 1380
gttncttaaa gtggtgtntc aagggnccta ca 1412

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<210> 50
<211> 866
<212> DNA
<213> Canis familiaris

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<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c, or t

```

```

<400> 50
ttnnnggaacn gcttgccaaa cctacagggtg gggcttttca agatctgctg acagtgaagc 60
taaactctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc 120
tcttaaaciaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttta 180
ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc 240
ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag 300
aaaaacatcc cgtgggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc 360
aggtcttgaa atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt 420
cagtaccaga gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat 480
tccagatacg atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt 540
attttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa 600
aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag 660
ttacaataga acaacgatag atctctaagg ggagagtgaaggacaccaa tttgagaaac 720
gtgaggcagg aaaagtttca aataattata ttcagagtgn tacctaagtt gttacttaaa 780
gacattctct acgtaaaana aacaataagg ccaaatgaag gaatgagagt tatgttatcg 840
cagaacaan gtaancgnt tntttt 866

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<210> 51
<211> 597
<212> DNA
<213> Canis familiaris

```

<220>
 <221> misc_feature
 <222> (1)..(597)
 <223> n is a, g, c, or t

<400> 51
 acacagcaat tcattncaat gaactgttat ggggtctcac attgtaccag gcaactgggga 60
 ttcagcttcc agttcatagt ctgcatgcaa accgacatgc aggtagacat gcagacagaa 120
 aatcggaacg caacacggta agtgctatgc tagagaatga gaaggactgt cagtaatcac 180
 aaccaccttt cactgggttc cttcagtgtg ccaggctcgt gtacattatt ttgttttagtg 240
 ctcaaatg tatggactgt gtactatcat ttgccagatt atatggatga agaaactaga 300
 ctgaggggggt taaataactc gtccaagatc atgcagacaa aaaaccacag agattatatt 360
 ccaatacaaa ctctctggct gtacagctca agttcttaaa cactggggcca accagtctga 420
 atctgagagg aggcattcta aggcttacag gtaagtggga attgaaaggg ttgaggggaag 480
 ccttctggag gagatgccat tacactgaat gttgaatgag taggagttag ctatctccag 540
 aggggtagtg gctgtgaagg ggcgaggggt agagggtggg aaggggatga tggaagg 597

<210> 52
 <211> 875
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(875)
 <223> n is a, g, c, or t

<400> 52
 cgcttgccaa cctacagggtg ggggtcttca agatctgctg acagtgaagc taaatctggc 60
 ggaagcaaa gattcacttt ctcataatgg attaactcat cctatttgcc tcttaacaa 120
 tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa ggatgcctat 180
 tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc ttggtaggag 240
 tatgcaggag gtcattttaa agccagatag tgatacaaat cacaatgcag aaaaacatcc 300
 ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc aggtcttgaa 360
 atctttaaat aatctacat gttctttggc ctgccctggg aaatctattt cagtaccaga 420
 gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat tccagatacg 480
 atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt attttggag 540
 taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa aatataaaca 600
 ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag ttacaataga 660

acaacgatag atctetaagg ggagagtgaaggagacctcaa tttgagaaac gtgaggcagg 720
 aaaagtttca aataattata ttcaagagtg ttacctaatg tgttacttaa agacattttc 780
 tacgtaaaat aaacacataa ggccaaanga agggaaatgag anttangtta tngcaggana 840
 aaaggtaaataat cggnntttttt ttgtatccat tgcaa 875

<210> 53
 <211> 612
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(612)
 <223> n is a, g, c, or t

<400> 53
 agcggataac aatttcacac agnaattcat tcaatgaact gttatgggggt ctcacattgt 60
 accaggcact ggggattcag cttccagttc atagtctgca tgcaaaccga catgcaggta 120
 gacatgcaga cagaaaatcg gaacgcaaca cggtaagtgc tatgctagag aatgagaagg 180
 actgtcagta atcacaacca cctttcactg ggttccttca gtgtgccagg ctcgtgtaca 240
 ttatttttgtt tagtgctcac aattgtatgg actgtgtact atcatttgcc agattatatg 300
 gatgaagaaa ctagactgag ggggttaaat aactcgtcca agatcatgca gacaaaaaac 360
 cacagagatt atttttccaat acaaaactctc tggctgtaca gctcaagttc ttaaactgt 420
 ggccaaccag tctgaatctg agaggaggca ttctaaggct tacaggtaag tgggaattga 480
 aagggttgag ggaagccttc tggaggagat gccattacac tgaatgttga atgagtagga 540
 gttagctatc tccagagggg tagtggctgt gaaggggcga ggggtagagg gtggnaaggg 600
 atgatngaaa gg 612

<210> 54
 <211> 732
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(732)
 <223> n is a, g, c, or t

<400> 54
 agcttgccaa acctacaggt ggggtctttc aagatctgct gacagtgaag ctaaatctgg 60
 cggaagcaaa ggattcactt tctcataatg gattaactca tcctatttgc ctcttaaaca 120
 atgggtattt taaagacaga agttgaagga agtccaagta tccaatttta aggatgccta 180

ttagagcagt tataagagag tgtctctctt tctctctctt cttctcttct cttggtagga 240
 gtatgcagga ggtcatttaa aagccagata gtgatacaaa tcacaatgca gaaaaacatc 300
 cccgtggact cctccctgtc ctatgtttga cattcttaaa atctatgtcc caggtcttga 360
 aatctttaaa taatctacca tgttctttgg cctgccctgg gaaatctatt tcagtaccag 420
 agctatgctg gttacacacc ttttctgact catgttcnca agtgatttta ttccagatac 480
 gatttgggga cagttacgtg tactgttctg atatcttcct aaaaggaaat tattttggaa 540
 gtaaagtcac tgataaaatc aactcaggaa aatgcacttt gtaaataatta aaatataaac 600
 attattaaag gccatgctgt aaaaaactaa ttgattttcc tgtgtagcag ttacaataga 660
 acacgatgat ctctaagggg agagtgaag gaccttattt ggtaaccgtg aggcagnaaa 720
 gtttcaaata tt 732

<210> 55
 <211> 697
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(697)
 <223> n is a, g, c, or t

<400> 55
 ctagcttgcc aaacctacag gtggggtctt tcaagatctg ctgacagtga agctaaatct 60
 ggcggaagca aaggattcac tttctcataa tggattaact catcctattt gcctcttaaa 120
 caatgggtat tttaaagaca gaagttgaag gaagtccaag tatccaattt taaggatgcc 180
 tattagagca gttataagag agtgtctctc tttctctctc ttctttcttt ctcttggtag 240
 gagtatgcag gaggtcattt aaaagccaga tagtgatata aatcacaatg cagaaaaaca 300
 tccccgtgga ctctccctg tcctatgttt gacattctta aaatctatgt cccagggtctt 360
 gaaatcttta aataatctac catgttcttt ggctgacctt gggaaatcta tttcagtacc 420
 agagctatgc tggttacaca ctttttctga ctcatgttcc caagtgattt tattccagat 480
 acgatttggg gacagttacg tgtactgttc tgatatcttc ctaaaaggaa attattttgg 540
 aagtaaagtc actgataaaa tcaactcagg aaaatgcact ttgtaaatat taaaatataa 600
 acattattaa aggccatgct gtaaaatact aattgatttt cctgtgtagc agttacaata 660
 gaacacgata gatctctang gggagagtga aaggact 697

<210> 56
 <211> 617

<212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(617)
 <223> n is a, g, c, or t

<400> 56
 tggattgcga gcgataaca atttcacaca gaattcattc aatgaactgt tatggggtct 60
 cacattgtac caggcactgg ggattcagct tccagttcat agtctgcatg caaaccgaca 120
 tgcaggtaga catgcagaca gaaaatcgga acgcaacacg gtaagtgcta tgctagagaa 180
 tgagaaggac tgtcagtaat cacaaccacc ttctactggg ttccttcagt gtgccaggct 240
 cgtgtacatt attttgttta gtgctcacia ttgtatggac tgtgtactat catttgccag 300
 attatatgga tgaagaaact agactgaggg gggttaaataa ctctgccaag atcatgcaga 360
 caaaaaacca cagagattat ttccaatac aaactctctg gctgtacagc tcaagttctt 420
 aaacactggg ccaaccagtc tgaatctgag aggaggcatt ctaaggctta caggtaagtg 480
 ggaattgaaa ggggttgaggg aagccttctg gaggagatgc cattacactg aatgttgaat 540
 gagtaggagt tagctatctc cagaggggta gtggctgtga aggggagagg ggtagagggt 600
 ggnaagggga tgaattg 617

<210> 57
 <211> 803
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(803)
 <223> n is a, g, c, or t

<400> 57
 cctgcagcta gcttgccaaa cctacagggtg gggcttttca agatctgctg acagtgaagc 60
 taaatctggc ggaagcaaag gattcacttt ctcataatgg attaaactcat cctatttgcc 120
 tcttaaacia tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttta 180
 ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc 240
 ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag 300
 aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc 360
 aggtcttgaa atcttttaaat aatctacat gttctttggc ctgccctggg aaatctattt 420
 cagtaccaga gctatgctgg ttacacacac tttctgactc atgttcctca gtgattttat 480

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tccagatacg atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt 540
atatttgaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa 600
aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag 660
ttacaataga acaacgatag atctctaagg ggagagtgaaggacaccaa tttgagaaac 720
gtgaggcagg aaaagtttca aatattatat tcaagagtgt acctaagttg ttacttaaag 780
acaattctnc acttaaataa acc 803
```

```
<210> 58
<211> 786
<212> DNA
<213> Canis familiaris
```

```
<220>
<221> misc_feature
<222> (1)..(786)
<223> n is a, g, c, or t
```

```
<400> 58
gngnggnaat gtgcagncgg ntaacaattt cacacagnaa ttccatttcc ctcaacaagc 60
aggagaaatt ttctcaagag ttaccagaa gtcactctta acgtcaggct tgcaaatttt 120
aaaaagcatg aaaaagaacg tctactacat aatcctccag gcacattcca acacgtgcc 180
aacagtattc ctgaaaatcc tctgtcaaac ccctccataa atcatagcct cagagctctg 240
tgtgtgtggc tgcagcaggc tcgtagctgc agagcacttg catggaggag acatgcgctc 300
aggaactgca ccgccgcatt ccgcagaagc cagcgactt acttccctct gctgcatgtt 360
aacctgtgct atgttctaga tcttacttta gttagtaatt caacaacagg agtcatgtgg 420
gctggcaagt agtcagctga aaactaacat gtgaacagaa ctctcagggg caggcctcca 480
gcaagctccc acccgagtcā gtactgctcc cgccttcctt tcagcttgtg ggtgggtact 540
accttctgaa gcctcacaaa acccccatct gaaagaagag gaaactgaga cacggtgaga 660
catggtgccc ctgccccaaa gtctgacagt ttgatatggt agagccagga atccatccca 720
gggnagtggg ccagaaggta gtggctgact gccatgccg aggacgtccc caggagctgc 780
cgtgaa 786
```

```
<210> 59
<211> 837
<212> DNA
<213> Canis familiaris
```

```
<220>
<221> misc_feature
```

<222> (1)..(837)

<223> n is a, g, c, or t

<400> 59

| | |
|--|-----|
| tctggnnccc cgggacgtnn ttgggagctg ccctgagctc ccacctgctg ctgccagtac | 60 |
| tagcacaggg tcctcaagtg atggctgctg gtgaattatt tagaatctcc atgggcaggg | 120 |
| cattctgctt tttagcactg tgtcttgacc tgttccaaga ccatcttcca aggagagcca | 180 |
| gcagctgggtg ttgtaagttc ttcccatgac aaataagccc aagacctcac ttaggaaaca | 240 |
| tacaatgatt atatgatctt gggagtcagc cctagaaggg cccttcttct cttgcttcaa | 300 |
| gctaaaaaga ctctggacaa caaaagaggc agtggctgct aagtaacttg caactaccac | 360 |
| ttcagtctca ctgcagctgc aaagatagga acagagaagt tttagggtgag aaactccttt | 420 |
| ttcccaagaa actgtgatga accagtgtta cagtttaggg agagagctct gtagacaagg | 480 |
| agggacctaa ggacccccag gactcaccac cccacacct agctcccctg gtcacctggt | 540 |
| acgtaagcag gtaggctctg cttagcatag tgctaagatc acatcttgct cagagtgtac | 600 |
| aaactcagga aagctggcat taggtagtat cacaagtga aaaatactc aaccagtggc | 660 |
| cattggaagt gcggaagtac atgccatact cactgcaagg ttctccattc cagctgccgt | 720 |
| actgtgtaat acgacttaat atcttcagag natcaagggt aatttcaa attggtgtcttc | 780 |
| aaagaacatt tctttttnt tcttttgggg ncagtactgc gcacatttta actagga | 837 |

<211> 866

<212> DNA

<213> Canis familiaris

<220>

<221> misc_feature

<222> (1)..(866)

<223> n is a, g, c, or t

<400> 60

| | |
|---|-----|
| ttgtcgagcg gataacaatt tcacacagna attccagcac catgcactct ctgagacagg | 60 |
| tgaggatttt gcagcagctg ataaggacac aagtgaacag gagcataata atgaaaacac | 120 |
| aaagactagt tagctgttac tacttgcttc tagggcttct agtgttctct gttgtgatac | 180 |
| ttgggtcaa at gttgtttggg agtcactgaa gaatgcttca tcatttgcaa agataggacc | 240 |
| ctaacttgta agccccttaa attaaaagaa tgcttttttag tacaaaatta atgatcttag | 300 |
| tcacaaaaag caaagaagaa atcaaaatca caaagtcac attcaaagtt gtattcttta | 360 |
| tagcaaaaat ggggcaagct acaggattgc caaagctct ataaaacagg aggaaggttt | 420 |
| atgaaatgat gctcagagag aatgcagaat gtgctattag cacaaatcct ttctgaaatg | 480 |
| gaacctgagc aaagtgatgg catttgatgt agaggaatag ccaccatcac atatgtgtga | 540 |

gagaaaaatag tttgcttctgg ggatgaacaa taccaccgtt gtacaaagca tgaataagca 600
 cttggaaaat gtatagtatg tataacagag ggacttttat ctgtttggca ttgaaaatca 660
 atgccattaa aagtaggaac aattggttat tgggnctgat tttttaaag aattcattta 720
 tttnttttng gggganagaa ncccccccc cctntnacc cnggggaaan annnaggggn 780
 aaaaaanaat nttnagccna ctnttttctt nntgggnccc cgggnngggg ctttancnca 840
 aancccnnga aannannntn ngncen 866

<210> 61
 <211> 886
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(886)
 <223> n is a, g, c, or t

<400> 61
 ttgngaaccc gcttgccaaa cctacagggt gggcctttca agaacataag cccaaataag 60
 cactggcaca tagtaggagc agcataaacg ctccccctcc tattcctaac ccaccaagaa 120
 ttctagattg acagtttttt ctttgagtat tttaaagatg ctgcttcctt gacttcttgt 180
 ttgcaaattt ctgatgagaa atctgctgtc attttatctt ccttcctttg cataatgatg 240
 tatctttttc tctctgcttt taagattttc attttatcac tggttctaag caatttaatt 300
 atgatgttcc ttggtatagt gctcttcata tttctattag gagtttggtg agcttcttgg 360
 atttgtgagt ttatagtttt tatcaaattt ggcaagtttt cagctactat ttcttcaact 420
 ttttttttcc tgtcctccct tgactcctcc tcattcccat atttctcctg tccttcaggg 480
 actccagtta tctgtatggt aagctcattg ataccctatt tgtgtatatt ttaaggcttt 540
 ttattccctg tatttcattt tggatagttt ctactgcaat gttttcaggt tctttaacct 600
 cttttttttt ttccccccag taatgtctaa tctgctcttc atcccaaaga catgtagtgg 660
 tgtgtgtgct aaaaatccca gacaatgttt ttatgattcc taggtatttg ctttggggct 720
 tttcaaagat tttccatatt tctacttctt tggccatata gaatgcggnt attattattt 780
 tttagnggcc tatgctacta aatccataaa ttntctggac tcnnttgatt nagnntnncc 840
 tttttattta ttnattaagn anggttttat tgggagttng attncc 886

<210> 62
 <211> 728
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(728)
 <223> n is a, g, c, or t

<400> 62
 ggattgtcag cggataacaa ttccacacag aattcccagg acccagcatg atgcctgggtg 60
 tgcacatggg tgggccctcc tatgtaagcg tcaccactcg ggagcagtgg cggggatgcc 120
 tggatgcgcc ggctcctgcy tgtagggtgc tatcaggaca ttgctgggtt gccacctctg 180
 tctgaggctc cagagagcga ggggacaccc cacatcatga atgccctgtg gggttaccag 240
 tgggggcaat tacctgcatt gctcctgggc ctacgcggcc tcactctgtga aatgggtaca 300
 ttcatatcac gtatgggaga gggctgccgt ggggtttaat ggaggcaacc catttgagcg 360
 ctgggcccgg caccgctcct gctcttactg tgactatggc cagcgtcact gttgcagggc 420
 cttgaccggc cgggggtggac gctgggtgcc cgtttgctct ctcccagggt gggaggagac 480
 aggcctgcgg ggcggactca ccgtggcggt gacggtgagc tggtaggcct gcgtgggtctc 540
 gtagtccagc tcgcggacca ccgtgacgat gccgcgggcy ctgtcgatgg cgaacaacgg 600
 ggaccggggc tggaaaggagt acaggacgct gcccctgca ccaagtcggg gtccgtggcg 660
 ttacgataaa atgggtgtcc ccaccggcgt gttctggggg ccaagcaaac aaccaagggt 720
 agtgggct 728

<210> 63
 <211> 785
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (1)..(785)
 <223> n is a, g, c, or t

<400> 63
 attgtcgagc ggataacaat ttccacacaga attcctaaaa cccttactgt tgtttttata 60
 tggcacttcc tgatgtgatt gcaggctttt agcaaagcca tttttgttaa caaaaaatga 120
 tttaaattct tttaaacaag tgtttagtga caagtcagta tttagtcatc tagttattga 180
 tacagcacc ataaaattta tcaactgagg gagggatcag gaggaaatgt gggcattcta 240
 acttaatgat taataatatg tgtctataac aaatgtgatg gctaagttat aaaatattta 300
 aaaaattttt tcttgcagg atttataaca gcaatgatgt agcagtatca tttccaaatg 360
 tggatatctg ctccaggatct agcactcctg tctccagttc tcatttacct cagcagtctt 420
 ctgggcattt gcaacaagtg ggagcactct ccccatcagc agcatcatct gcaaccctg 480

```

ctgttgetac aaetcaggta atcattacag tgctatgaag taacctgtag atggccttgt 540
cgtttttgaa agtgagtttg attggagaag aaagaaacct tgtatagaaa ccttcctata 600
taaattccta taggaattta taagtatctc catttgtttt gacacgtag taggataaat 660
agacattttt atgtgatatt catgagaaag gacaaaagaa tacattggca ttaactgatt 720
cttttcagtt tctgagtttc taatttttcc tgaagatgna aacaaaaatt tggggggaac 780
tttta 785

```

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<210> 64
<211> 981
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(981)
<223> n is a, g, c, or t

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```

<400> 64
ttgnaancg tcagaccaag tttactcata tcggatccaa agtgcttgag actgcatttt 60
tttcaaatTT tgcaatatTT gcattataat caccagttaa gcatccgtaa tccaaaaatc 120
ctaaacctac aatgctctaa taaatatttc ctttggctgt gttggtgcaa aaaatgtttt 180
ggattttgga agacttcaaa tttcacatta gggataccct gagtggaaaa aatagttttt 240
gtttttaaga ttcttttact caacaacaat caacaaggta gacttctgtg atcaaatgtg 300
tgaggatttc tccccaccaa taagcaatca attctgcagc agacaccaag tgggtatcct 360
ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct 420
cagtcccaca agactgctcc ctacttctga tgtcaatcac aagccacagt ttgttttacc 480
tgtgcttcta actgactgga tataaactgg gaatctcatg agcccctctt tgggttcggg 540
taatttgcta gagtggctca cagaactcag ggaatcacat ttattagttt attataaagg 600
atatacagtt gaagagatac acatggcaag gtatgccctc cctgggaaca ccactctcca 660
ggaacctnct tttgttctg tccagaagct cttcgaatcc tctcctcttg ggccttttat 720
ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat 780
atatgatcta atattaatag actggggaaa ctcanaggg cctgtntgtt caaatnttc 840
ngnctntttt gggtagcatt ncttntctca gggttngggg gngnacnttt ttgaaagaaa 900
gtntttgacc ctanncaaaa gngggggaag annaantnct ctttnggcag nnaaaaaaaa 960
aaaaattttt ttttnggnt n 981

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<210> 65
 <211> 981
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(981)
 <223> n is a, g, c, or t

<400> 65
 ttgnaancg tcagaccaag tttactcata tcggatccaa agtgcttgag actgcatttt 60
 tttcaaattt tgcaatattt gcattataat caccagttaa gcatccgtaa tccaaaaatc 120
 ctaaacctac aatgctctaa taaatatttc ctttggctgt gttggtgcaa aaaatgtttt 180
 ggatttttga agacttcaaa tttcacatta gggataccct gagtggaaaa aatagttttt 240
 gtttttaaga ttctttcact caacaacaat caacaaggta gacttctgtg atcaaagtgt 300
 tgaggatttc tccccaccaa taagcaatca attctgcagc agacaccaag tgggtatcct 360
 ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct 420
 cagtcccaca agactgctcc ctacttctga tgtcaatcac aagccacagt ttgttttacc 480
 tgtgcttcta actgactgga tataaactgg gaatctcatg agccctctt tgggttcggt 540
 taatttgcta gagtggctca cagaactcag ggaatcacat ttattagttt attataaagg 600
 atatacagtt gaagagatac acatggcaag gtatgccctc cctgggaaca ccactctcca 660
 ggaacctnct tttgttctg tccagaagct cttcgaatcc tctcctcttg ggccttttat 720
 ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat 780
 atatgatcta atattaatag actggggaaa ctancaggg cctgtntgtt caaatnttc 840
 nggncntttt gggtagcatt ncttntcca gggtnnggg gngnacnttt ttgaaagaaa 900
 gtntttgacc ctanncaaaa gngggggaag annaantnct ctttnggcag nnaaaaaaaaa 960
 aaaaattttt tttttnggt n 981

<210> 66
 <211> 1005
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(1005)
 <223> n is a, g, c, or t

<400> 66
 ctnagctngc ttgccaaacc tacaggtggg gtcttttcaa aaacagacat gcagacttta 60

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acagataata aggttttttga ggttttccgt ttatgtattt actcgagaaa gcaagagctt 120
tatttattta tttttgagac ggagtttcgc tctgtcgccc gggctggagt gcaatggctc 180
catctcgtct cactgaaacc tctgcctccc gggttcaagc gattctccca tctcaacctc 240
ccgagtagct gggattacag gcgcgcgacg ccacgcctgt ataaaaatac taaaaatgca 300
aaaataatth ttgtatthtt agtagagatg gcgtttcatc atgttggcga aactccaggc 360
tggtctcgaa ccctgacctc ggtgatctgc ccgcctcggc ctcccaaagt gctgggatta 420
caggcgtgag ccaccgcgac cggccaagag ctttataaag atggaaaacg aagcagactt 480
tctgcccag ccattgctttt ggataaggat tacactactt tgaaatctta catatatagc 540
acttggccaa ctatcaaaac tgcacaaacc ttcactaatt gcaattattc cctttaacat 600
ctcgagttac cccaatccgc acaaaacaag tttagtgcgc accaggtaat aatacattca 660
ggaaaataat tccaagaaca gacgtttaag aactacagag aaaaacatac ttttttctac 720
aagaaaaaat cttagaggac agtaccaggg nccttatctc tgttagcatg atttatatth 780
cacgtaacgt tggcccagtc actgctncat tntaaancna tagccanggc anatagaaag 840
tctgaacana ttgacngcna ngggttttaa ttttttacca ggnaacaaan cctggcaaac 900
tgccancang ggtgccc aaa tgctggnctn gggtccttg aagnaacgg agggctttga 960
atthttttcc ntttngaac ngncnngnt ttnggcnaa thnttc 1005

```

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<210> 67
<211> 863
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(863)
<223> n is a, g, c, or t

```

```

<400> 67
nttttggng nntancttnt ananatnngc caattattgg ggggnacctt catcataagt 60
attaatataa taataataat aagtaatagt aactagtaac aacaataaaa aggaaatcag 120
cggaaagtca ggaaaaatgt taaaaaaaaa ttggaataac ttactgtagc tgaagatcaa 180
aaaaatctca ctgtaaaaaa acaaaaataa aaatagccca gattagaaaa acggggagtg 240
caaaaatgtc aagtcagtaa agttcatttc ttttctcttt ccaaaagcag tttccacaaa 300
aaccgcaagg ataaagttht cagtagcaga caagcaaagc cctttcgaca tcatcaatca 360
atcttaaaaa tacacgagga agtagagagg tcagtttatg agaggctaaa aggctcctcc 420
tcctctaacc caactgctgc agaaaaata gaaatagaaa ttttaaaaat tacatcttaa 480

```

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| | |
|--|-----|
| atccagggtcc cggttttggg aacaattaaa aaaaaaacac ctgtacattt gccgtagtgc | 540 |
| acaccaagtt gcatcattat gtttaaatg tctttataaa atcagttttg gaatggaatg | 600 |
| tgtgtgttct ggaaggggtg ggaagggagg ttaaaaatca aagctgagct ccagtgaagta | 660 |
| gggatggggt tcgccttgct gccctgtgaa agggaaagga cagatnagtc aanttntctaa | 720 |
| aaatgtntgc cctaancccn anaaaaaact ttgnntttng aantaaaaat ttggtgaagct | 780 |
| ttaaattccc tggnggggaa nccnctntaa naccttttca ngnnngntta aaattttaan | 840 |
| aaaanggggn naaaaaaaaa ncc | 863 |

<210> 68
 <211> 918
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(918)
 <223> n is a, g, c, or t

| | |
|---|-----|
| <400> 68 cnnnttctgg nngatnaaan tnnttnnnna nttcnccaat nnattggggg gaannnttca | 60 |
| tcataagtat tnatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag | 120 |
| gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaatt ggaataactt actgtagctg | 180 |
| aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac | 240 |
| gggaggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagcagtt | 300 |
| tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc tttcgacatc | 360 |
| atcaatcaat cttaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag | 420 |
| gtctctctc ctctaaccce actgctgcag aaaaaataga aatagaaatt ttaaaaatta | 480 |
| catcttaaat ccagggtccc gttttggaaa caattaaaaa aaaaacacct gtacatttgc | 540 |
| cgtagtgcac accaagttgc atcattatgt ttaaaatgct ttataaaaat cagtttttgg | 600 |
| atggaatgtg tgtgttctgg aagggtgggg aaggagggtt aaaaatcaa gctgagctcc | 660 |
| agtgagtagg gatgggggtc gccttgctgc cctgtgaaag gagaaggac agattgagtc | 720 |
| agagttcctc aaaaatgttg tgccctaaac cccaagaca gaaacatctt gtttatntn | 780 |
| gctaacacaa tntttntgna naatnatnaa cctccccngg ggagggnacn ccctnnnnaa | 840 |
| aannnccctt nccanggant gnnttnaaan tttttnaana tnantggggg nanaaaatna | 900 |
| acnaancctt gnnaattn | 918 |

<210> 69

<211> 887

<212> DNA

<220>

<221> misc_feature

<222> (1)..(887)

<223> n is a, g, c, or t

<400> 69

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tncantcttt nnnnggcna nacgcgcgc nantcgccaa tnactggggg ggnancttca      60
tcataagtat taatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag      120
gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaaatt ggaataactt actgtagctg      180
aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac      240
gggagggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagcagtt      300
tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc tttcgacatc      360
atcaatcaat cttaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag      420
gctcctcctc ctctaaccce actgctgcag aaaaaataga aatagaaatt ttaaaaatta      480
catcttaaat ccagggtccc gttttggaaa caattaataa aaaaacacct gtacatttgc      540
cgtagtgcac accaagttgc atcattatgt ttaaaatgtc tttataaaat cagttttgga      600
atggaatgtg tgtgttctgg aaggggtggg aagggagggt aaaaatcaaa gctgagctcc      660
agtgagtagg gatgggggtc gccttgctgc cctgtgaaag gagaaggagc agattgagtc      720
agagttcctc agaaatgttg tgccctaacc cccaagacag aaacatctgt ctttgagct      780
aacacatttt ggnaagcatn acatncaactg ggatggacag ccncntaaaa aaccttnncn      840
ngncnnnttt naanttttaa nnnaaagggg nnnaaataan naaccn                      887

```

<210> 70

<211> 897

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(897)

<223> n is a, g, c, or t

<400> 70

```

ctttggggng tnnttcanac nttttancac nntnntcgcc antccncttg aggggnaaac      60
ccatgcctt ctatcgnctt cttgacgagt tcttctgagc gggactctgg ggttcgaaat      120
gagctagccc ttaagtaacg ccattttgca aggcattgaa aaatacataa ctgagaatag      180
aaaagttcag atcgagggtc ggaacagatg gaacagggtc gaccggtcga ccggtcgacc      240

```

ctagagaacc atcagatggt tccaggggtgc cccaaggacc tgaaatgacc ctgtgcctta 300
 tttgaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc tccccgagct 360
 caataaaaga gccacaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc 420
 cgggtaccgc tgtatccaat aaaccctctt gcagttgcat ccgacttggt gtctcgctgt 480
 tccttgggag ggtctcctct gaggattga ctaccctca gcgggggtct ttcaatgatg 540
 gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagtttttc 600
 tgaatgtttc taagaatttc tccggcctcc tgattgactt tggagttttg catcttggga 660
 gagaaagcga aggcattagt atttttaagt ggattgatca cataaacctt ttctctccca 720
 accccaccct tgccttcttc cccttcccca cactgaacag aattttactg gctgntaagt 780
 ctatgacctt attttttctt gatctttaac ttaactgntt tagagcatct ntggacgncn 840
 ggattttnaa attttttnat tttnggnttt ttnntttnaa annttnnatt gggaaan 897

<210> 71
 <211> 878
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(878)
 <223> n is a, g, c, or t

<400> 71
 tcggggngnn ctccactnnt gntgcnnntc nncgccantc cnettgnggg gnaaaccatc 60
 gccttctatc gnetttctga cgagttcttc tgagcgggac tctgggggttc gaaatgagct 120
 agcccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag aatagaaaag 180
 ttcagatcga ggtcaggaac agatggaaca gggtcgaccg gtcgaccggt cgaccctaga 240
 gaaccatcag atgtttccag ggtgccccaa ggacctgaaa fgaccctgtg ccttatttga 300
 actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata 360
 aaagagccca caaccctca ctcggggggc tagtctctcg attgactgag tcgcccgggt 420
 acccgtgtat ccaataaacc ctcttgaggt tgcacccgac ttgtggtctc gctgttctct 480
 gggaggggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa tgatgggtgat 540
 gatgatgatg ataataacac tgatgatttt taaccggatt aaaatcgagt ttttctgaat 600
 gtttctaaga atttctccgg cctcctgatt gactttggag ttttgcatct tgggagagaa 660
 agcgaaggca ttagtatatt taagtggatt gatcacataa accttttctt tnccaacccc 720
 acccttgccc ttatcccctt ccccaactg aacagaattt tactggctgn taagtctatg 780

accttattttt tcctgatctt taactnactg ntttagannt ctctggacgn cggnnntttna 840
aatttnttat tttgggtttt tantttaaan cttnattn 878

<210> 72
<211> 964
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(964)
<223> n is a, g, c, or t

<400> 72
cttctggggnn gannnaanca nttegnncan nnctccncca atctacttgn ggggcaaacc 60
catcgccttc tategttctt cttgacgagt tcttctgagc gggactcttg gggtcgaaat 120
gagctagccc ttaagtaacg ccattttgca aggcattggaa aaatacataa ctgagaatag 180
aaaagttcag atcgagggtca ggaacagatg gaacagggtc gaccgggtcga ccgggtcgacc 240
ctagagaacc atcagatggt tccagggtgc cccaaggacc tgaaatgacc ctgtgcctta 300
tttgaactaa ccaatcagtt cgttctctgc ttctgttcgc gcgcttctgc tccccgagct 360
caataaaaga gcccacaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc 420
cgggtacccg tgtatccaat aaaccctctt gcagttgcat ccgacttggt gtctcgctgt 480
tccttgggag ggtctcctct gagtgattga ctaccctgca gcgggggtct ttcaatgatg 540
gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagtttttc 600
tgaatgtttc taagaatttc tccggcctcc tgattgactt tggagttttg catcttgggg 660
gagaaagcga aggcattagt atttttaagt ggattgatca cataaacctt ttttttncca 720
acccaccct tgncttatn cccttnccca cactgaacag aaanttactg gctggnannn 780
natganccta nttttncn gn ncttnaanta acnggnnnna anaaancnng gcnncccggn 840
nnnaaaaaan ttnnnnnnng nngntttttt naaaaancnt nnttnnaaaa ntaaaancgg 900
nnnnnaaaaa nggggggggn cnnncnancn tnannnnggg ngggttttcc nnnaancntt 960
ttcc 964

<210> 73
<211> 986
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(986)

<223> n is a, g, c, or t

<400> 73

```

catcnttctg nnnngnaana aacgtncnnn nnncnctcc cnaatttaac ttgggggggn      60
aaaancatcg ccttctatctt ttcttcttga cgagttcttc tgagcgggac tctgggggttc    120
gaaatgagct agcccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag      180
aatagaaaag ttcagatcga ggtcaggaac agatggaaca ggtcgcgacc gtcgaccggt      240
cgaccctaga gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg      300
ccttatttga actaaccaat cagttcgcctt ctgccttctg ttcgcgcgct tctgctcccc      360
gagctcaata aaagagccca caaccctca ctcgggggcg cagtcctcgc attgactgag      420
tcgccccgggt acccgtgtat ccaataaacc ctcttgcaat tgcacccgac ttgtgggtctc    480
gctgttctctt gggagggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa      540
tgatggtgat gatgatgatg ataatgacac tgatgatttt taaccggatt aaaatcgagt      600
ttttctgaat gtttctaaga atttctccgg cctcctgatt gactttggag ttttgcattct    660
tgaggagaaa agcgaaggca ttagtatttt taagtggatt gatcacataa accttttctc      720
tcccaacccc acccttgccc ttatcccctt cccacactg aacagaattt tactggctgt      780
taagtctatg accttatttt tcttgatctt taacttaact gntttanagc atctntggac      840
gnnngnattt naaanntttt tatttngnt tttnatTTta aannttnatt ngnaaanntt      900
naactgggct gnanaaaagg gnggggncta ctnaaantnn nnacgggagg gntttncctg      960
nanncanttn ctccnnttcc ntgaan                                           986

```

<210> 74

<211> 748

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(748)

<223> n is a, g, c, or t

<400> 74

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ttttttgcnt taccgtatcg ccgctnncga ttgcagcgc atcgcttct atcgcttct      60
tgacgagttc ttctgagcgg gactctgggg ttgaaatga gctagccctt aagtaacgcc      120
atTTtgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg      180
aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgtttc      240
cagggtgccc caaggacctg aaatgaccct gtgccttatt tgaactaacc aatcagttcg      300
cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc      360

```

accctcttgc agttgcatcc gacttgtggt ctgctgttc cttgggaggg tctcctctga 480
 gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga 540
 cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc 600
 cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaag gcattagtat 660
 ttttaagtgg attgatcaca taaacnnttt tntcttccaa cccaccctt gcccttatnc 720
 ccttncccac actgaacaga attttact 748

<210> 75
 <211> 881
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(881)
 <223> n is a, g, c, or t

<400> 75
 tntcttgagg acccgatcg ccgcttcga ttgcagcgc atgccttct atgccttct 60

 attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg 180
 aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgtttc 240
 cagggtgccc caaggacctg aatgaccct gtgccttatt tgaactaacc aatcagttcg 300
 cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc 360
 tcaactcgggg cgccagtcct ccgattgact gagtcgccc ggtaccctg tatccaataa 420
 accctcttgc agttgcatcc gacttgtggt ctgctgttc cttgggaggg tctcctctga 480
 gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga 540
 cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc 600
 cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaan gccttantat 660
 tttttagnng gtnggnnaca tataaccttt tttttccaa nccccctt ncccttttnc 720
 cctttccccc actgaaaaaa attttacngg ctgnnaannn tnnnacntn ttttnccnn 780
 ncttnannna annggttnaa gaccnnnnng gccnnnggn ttnnaantt tttntttng 840
 ggnntttnt nttnaancnn cnttggnaaa ntttnaanng g 881

<210> 76
 <211> 906
 <212> DNA
 <213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(906)

<223> n is a, g, c, or t

<400> 76

```

cannnttctg gggngtnnnn aactnannnn nnnnatcgcn nccacantnn nnttgggggg      60
aaaaacctga atacatttgt ngttatttcc cttagatctt tttttttttt tttttttttt      120
ttgagacatc tcactctgtc acccaggcta gagtgaagtg gcacaatctc tggtcactg      180
caacccccac ctgcctgggt caagcgattc tcctgcctca gcttcccgag tagctggtac      240
tatagggtgtg caccaccaca cctggctaata ttttttaaaa aatattttta gtggagatgg      300
ggtttcacca tgttgaccag gctgggtctc aactcctgac ctcaaaggat ccacctgcct      360
tggcctccca aagtgtctgg attataagca tgagccacca tgccagcctg tttcttttag      420
atcttgattt gatattctgg atatgaatga aagaaaatta atgagtgttt caaagtctaa      480
ataaggaagc tccacagata atattaacat ttctctgac tagtcatatt tattattgtg      540
tttcaattag aagtggctgt aggtcttgaa agacacacta taaataaagc ctccccctca      600
tacacctca ctcacacca cacttacacc aatgcaattt tttagacagaa acacaagcaa      660
gaaataggat agattttttt taaaaaatgg gcattgggta aattttctgg tcatattaaa      720
aaanntnttt nagaactccc aanggggggc cattaataga gacctnattc nctgnnggaa      780
nnaaannggn aattnctnan aatnctnac aatntttagg ganttgangn aaaatnttnn      840
gtnnntgnaa ctttcctagn ggnctnnntn ngccctatnc ccaggnnttt tatnctaaac      900
ccntc                                           906

```

<210> 77

<211> 909

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(909)

<223> n is a, g, c, or t

<400> 77

```

cntcttnngg gngttnaanc tgnctnnaa tgcntcacat tnattnnggg gaaaaccgta      60
ctgacttatt atgagagggt tctgtcttg ttaggatcca gtaggtttga ggtgcaacta      120
ttctctact ttactcttcc acctcccaga gaactctgcc aagaaccatg ttaagactgc      180
tttctgcttt aactactaat agtcttgatt ataggaacgg aatttggtga tcaagtaggt      240

```

```

tctaagaact taacataaaa actggctatt aatgcatttg caaaatttgc attttaaadc 300
caaggcaaga acaggtcagg caaaaatgga atccaaacac caaattgtta aaagttttaa 360
gtccatttct cttgttagtt tgcaacttaa attactaatt ctctaattgt ttagagcaga 420
agttggtaaa ttgtttctgt aaaaaaattg tttctttaaa ttgtttcata atcaaaattt 480
taggttgtgt aggtgatact gtttctgttg aaattattta atctaaataa atggacatag 540
ctgtgttcta acaaaacttt atgattaacc tgacaggcca gatttgaaat gtttagcagg 600
ttgcacaccc ctactttaga aaaactcagt ctttatagct tccagttaca agatgtatct 660
tttttttttt tttttttaaa taagacagta ttattncaaa tgtcgggttg ctcataccna 720
aattgttttc ccntttcttn anttttcnaa angtyggggc caaanacttn aaaaggtn 780
annnttttnn nntaanaaaa nanccattta ggggnttnn caaccctnn aaaaantttt 840
tttcttnaaa aanaantnca naaaannntn ctnaaaaaan naaagggggc caccnttnt 900
ttttaaac 909

```

```

<210> 78
<211> 890
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(890)
<223> n is a, g, c, or t

```

```

<400> 78
gnnntncnnc tttnnngat cagccgcnc ncagnncccc accaatccna cttggtgtaa 60
acccccagc agggctcttg gctttcttcc tgcttctcca aaatgggcct ggcttcccag 120
gagacagccg agagcgctc gccctgctg gaagggcagc ctgggagctg gagttggcaa 180
acgggagggg acgggaggag gcccgaggga gggggcgtct tcccttagct ttcagcgaca 240
tctgctggcc gtgcgctgaa ctgccgctac cccagaggcc agctggagac caattttgag 300
ttgtgagcag ggaagagag gaggggttcc aggacaatca ggtctggagc ttccagaaac 360
attccaaaaa cacagtttag gctttttaat tgttactca gtcattctcc cggggcttag 420
ggagaaatcg gactcagact cggatctttg gggacctacc gcagcatgat aaccaggty 480
tacctggggc tcatgggggc ctggggatca gggaggcccc tcacctgcat tcaactgtgt 540
ccaagcactg gcctacatca ctgacatttg ctgtctcgct gcgggtgctg tgatcttgct 600
gctgtgctca ttgacagat gaaaacgctc aggttgtgag agaaccceaa agccagagga 660
ttcccttgat cactccctt cgttcagcc catagtcaat ccttcttcaa agcctatccg 720

```

tcccacctcc aaagcacacc atggatgccc atccttgccc catcatcggt accctctnag 780
 tgccagcctg cctgancccc tcanttnaag tcccgcctcc tggccttttg cagaagcatc 840
 ccaccagaat ctncagcca cccctccna nttntntntt cccaaatggc 890

<210> 79
 <211> 965
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(965)
 <223> n is a, g, c, or t

<400> 79
 ntttctggnn gtnacagang gggngccnnn ccccccatn aactgggggn aaacncnccc 60
 agccccaagg tggccattgt cagggagggt cttgctatgc agatgtgccg ttcaaaggca 120
 tgcagatatg aaagcatcgc tccctcaggt gggagacaat gggaagggtg agagcactgt 180
 ggtagtaggc aaggcttttg aattagcagt ccctgcattc aaatcctagc ttactttgcc 240
 tcatgacagc cgtctgtcct tgagcaaaat tgtttaacct ctctggacct gtctatatct 300
 gtaaaaagg gccaacatggt gtacccaaaa gccttgtcgt ggtgatctca ttaagatatt 360
 tcatgtgaat atgtgctgag tggcctcacg taggagggtc ttactgactt ctccaagcc 420
 ccctcctctt catcgctact gccctgtcgc gtatcctcca gcctcctccc acgctttctc 480
 tcaactgact ttttgggggt gagggaggcc atttctgagt cacttgctcc tggacttgat 540
 gaattccatt cgtgtggcgg gggcagcagg gccagtggtg aaccagcagc tccccaaccc 600
 tgcccactat accactcaag tgagtccaag ctgtgatgcc cctggctgcc tccccactt 660
 cccttgagcg agctgggagg acaaagattg gactctgagg atcagcctga gacttaagat 720
 ggaggctgtg ttcccgagag cccagggtgg gcatgccagg aagcactctg gctccacgga 780
 atgtgact gccccggggc tggcanacca ncacttcctt gtnttntctg gtctnacagn 840
 cncancctgg cctgggctgt ttttgcntgn tgnacctgcc tnaaannggn aaancctgg 900
 ancctggagn ctccnaggt ttngnttttc caancncca aaatangnc naaccngnct 960
 nnggc 965

<210> 80
 <211> 891
 <212> DNA
 <213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(891)

<223> n is a, g, c, or t

<400> 80

```

tttggttaact gtcagaccaa gttttactca tatcggatcc tctctatcag attgatctgc      60
agggtgagggt gtccagagat gtcttgcaaa tggcaatgtc ccaggccatg gaaacaggaa      120
tatgggctca aatccattta tggccaggca tgggtggctca tgcctgtaat cccaacactt      180
tgaggagggtca aggcaggagg attgcttaag cccaggagtt caagaccgtc tgggcaacgg      240
agaggagacc ctgtctctac aaataattaa aaaattatct gagcatagtg gcacatgcgt      300
gtgggtcccag ctactcggga ggctgaagtg ggaggatcgc ttgaggccaa gaggtcaagg      360
ctgcagtga a ctgtgatcat accacggcac ttgagcctgg gcgacagagc aagaccctgt      420
ctttcttttt ttttttcaaa aaaaaaaaaat ccatttataa tttaacatgg gagcctcacg      480
ggaaagagtt cttgtcttgt tgagtgggtcc agtggttttg atgggctgga actttgcact      540
tgatgtgttg taattcattt tctagagtct atgtcgtgaa ggtccttggg gtgatagagc      600
cttgaaaaaa tgttgtttcc ctgtggatta tctaaactag atccaagaac atgaaagacc      660
atccctcagg gagctggcat ttgtctaaaa accancattn cctgggccat ttgattgggg      720
ntcttgcttc actgcaaang ggggacttgc aaaattttac tnatgnccn nttgtntttt      780
ttntccaagg ggnttttana aaatttttct tnnnnntttt nnnnaanacc cnttnnant      840
tntnttttnc nccccnttt nttntaacna nggggggntt ttnaacnncc n      891

```

<210> 81

<211> 803

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(803)

<223> n is a, g, c, or t

<400> 81

```

tggtaactgt cagaccaagt ttactcatat cggatccctt ctgggtccac atcactcagg      60
caactctctc tcccacctg cccccaaac tcccttcac ctccctccac atgtatctc      120
ccacttcctt ccactcatgt aatgagaggt gctgatgagt cacaggagag gtagccctag      180
ataaccaaca gactgcaaaa cggacagtcc ctggatgtct gagccagtgt ttgtgcactg      240
cattgactgg ctctcgtag ttttttcctg tagttgctaa agcctgtaag gtctgtgtga      300
tgaatatttt ctaacacatc ttagaagaac ataatgcaag acagaatgaa aaactagaga      360
ggcagaaacc ccaaagtaa gtagtgggaa attaccaggt atataatagg tcaagcctgc      420

```

```

tctgcaggag ctcaagggat tgtagcattc ttatcccaaa ceactgaatc ctgggcaaaa 480
ataagaagtc gcctaatttt agtattacca gcttccaac cccgggcatt ctcatctta 540
ctcaagctgt ccagaggccc cagggtgact ccctataagt cccatgggtg gctgagatct 600
atttagaggg acaagggtat ctccctataa gtcccatggg tggctgagat ctatgagaag 660
catcttgggg agagtgcctc tggccaccag catgtggccc tgaatctttc atgtgcaact 720
ggccagggaa ggaaattatg gaaatagtca tcctgcacat ntgcaaatga gatgcaaatc 780
ctggaagctc ttctaaaaaa aaa 803

```

```

<210> 82
<211> 763
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(763)
<223> n is a, g, c, or t

```

```

<400> 82
tcgtgcttta cggtatcgcc gctcccgatt cgcagcgcat cgccttctat cgccttcttg 60
acgagttctt ctgagcggga ctctggggtt cgaaatgagc tagcccttaa gtaacgccat 120
tttgcaaggc atggaaaaat acataactga gaatagaaaa gttcagatcg aggtcaggaa 180
cagatggaac agggtcgacc ggtcgaccgg tcgaccctag agaaccatca gatgtttcca 240
gggtgcccc aaggacctgaa atgacctgtt gccttatttg aactaaccaa tcagtctgct 300
tctcgcttct gttcgcgcgc ttctgtctcc cgagctcaat aaaagagccc acaaccctc 360
actcggggcg ccagtcctcc gattgactga gtgcgccggg taccctgtga tccaataaac 420
cctcttgagc ttgcatccga cttgtggtct cgctgttcct tgggaggggc tcctctgagt 480
gattgactac ccgtcagcgg gggctcttca gtagcccttc cttttagtag aagacagaca 540
gatgggtgat caagagatac gcaagaagag gaccgtgtgt gtaatggttg agctctaaaa 600
agagaaatca cttggatgga aatgaaggag aggaaaaggc tgatgtggat ggctgggaag 660
aggttcgatg gttaccttgg caaccgagct tctttctcat cccatccctt ccctagtcct 720
tgtcttaaaa gatttttttn tatgtccctt cctcccaag ggg 763

```

```

<210> 83
<211> 861
<212> DNA
<213> Cercopithecus aethiops

```

<220>
 <221> misc_feature
 <222> (1)..(861)
 <223> n is a, g, c, or t

<400> 83
 ttggggganc ctgtcagnac canttttact catatccgga tcctgacctt cattcagtgt 60
 tctagattga aatcacagat tttggataga gaaaaaaaaa tattctctgc aatctaataa 120
 aaccaacttt tttttttttt tttttttttt ttgagacaga gtcttgctcc atggcccagg 180
 ctagagtga gtagcacgat ctgggcttgc tgcaacctct gcctgtcggg ttcaaccgat 240
 tctctgtcct cctgtctcct gcccagcct ntcaagtagc agggattaca ggcatgtgcc 300
 atgatgcca gctagttttt tgtattttta gtagagatgg ggtcttgcca tgttgcccag 360
 gctggacttg aactcctgac ctccaggtgat caggccatct tggcctccca aagtgttggg 420
 attacaggcg tgagccatcc tgcctggcca aaaccagcat attttatgga taggaaattg 480
 gaccaaaggc gaattcttta ttgcaggctg tgggnttttt ccatgtggct ggtggnacac 600
 tgcaccaagc agcacacaca ctaggccagt ttncctttgca gaccagttg caatcccatc 660
 tntnagccag gattctatta ggtctcnaca accnatggga atttagggng ctcanagntt 720
 nnggggtgga aaaggggact aacctncntg ggttnanggn ttttnaantg gncncnncct 780
 ttggancngg ganattttatt nccaaaanng gnnnggntng tnttngggnn anaaaccaa 840
 ttttgggaaa aaancntttt t 861

<210> 84
 <211> 767
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(767)
 <223> n is a, g, c, or t

<400> 84
 ggnattgncn agcggntaac aatttcacac agnaattccg tatttgaaat ttggggacaa 60
 tcgcttgaat cttaaaatta cttttctggt cagcgcgccc gaaggtctaa gcatttgtga 180
 aatgtctttt ttccccccc ccacccttg atgctgttct ctttgggctg tcttaattac 240
 acaggggttg agaaaccaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca 300
 tgcttttagc tttgcttgtt gaagttgctt ctctccctg agtggctttc ctctttttt 360
 tttttttttt tttattttta aaaggaaata tcataagctc tttcagaaat actcacagga 420


```

agtgagtgtc cgtatgctgg ttactcacca gcaactgant gttggcaggt ggagaatgct 480
accgcancn cccanacaga tctgcaaact ggcccnttnc agangatnaa aacagggtgc 540
gtggaantan ggtttttggn naaangcant ttnaaagnaa atgggcactg cattnnnttc 600
nagggggggg anttaagnaa cangnttggg gtnaaaaagn ncntgnttcc attnnggngg 660
tnctgctcct ttnaaanggg nggnnggttt naaaaaaag ggcccccnc cccanaaaaa 720
aatttttttg nggaaacct nccaaaaaaa anaccccn cn tttttgn 767

```

```

<210> 85
<211> 761
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(761)
<223> n is a, g, c, or t

```

```

<400> 85
cngcttgcca acctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt 60
gtatgtatgt caaaacaaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat 120
atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca 180
tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg 240
ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag 300
tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa 360
gcgcaggact tgccttgaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa 420
atgccaaatg ccagcgtcc ctttnccag ctcatcttat ttgtaggcac tcagattttg 480
gaatcctcca ggactaacat taaaaccca ctagggngtt tncctaatnc cgggaaanga 540
gncagtaggn caaacaactt atccccncna nanaggaaca attccttgag ctccccnct 600
gtttcngaaa ccctnttccc ttntgggncc ctgnanaagg nctgcccnaa tgctnngggag 660
nccncnggt tttnatgaaa accatntnaa aatncccnaa agttncccc ccaaggnaan 720
nttcnttta aanttttggg aaaaaancc ccntnanaa n 761

```

```

<210> 86
<211> 791
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(791)

```

<223> n is a, g, c, or t

<400> 86

```

tnggggacca gcttgccaaa tctacaggtg gggctctttca aaatattgcg ttacaaatat      60
cattttggtg tatgtatgtc aaaacccaaa ctgcctttat gtcaatatgc tgtaaaaatc      120
tatcagaata tatcttaatt cttaactttc attgttgtct gtgggctgtc ttgtataacn      180
attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg      240
gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc      300
aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa      360
ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg      420
caagtagaaa tgccaaatgc cagcgctccc tttccccagc tcattcttatt tgtaggcact      480
cagatttttg aatcctccag gactaacaat aaaaaccaca ctaggttggt ttctaattc      540
ctgtgaaatg agtcagtagg tcaaacaact tatccactcc agagagagaa caattccttg      600
agctacactc cctgtttcca gtaaccctat tccctctctg tgtccctgga taaagtgtg      660
ncnacaatgc atgganagcc cccgggttct gatgaaancn atngaagat ngcanaaagt      720
agctgcctta agggaangtt cccttngaaa ttaggnaaa aaaanccnnt aaaaanacng      780
gnggtcgggt t                                          791

```

<210> 87

<211> 783

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(783)

<223> n is a, g, c, or t

<400> 87

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ttgggganca gcttgccaan tctacaggtg gggctctttca aaatattgcg ttacaaatat      60
cattttggtg tatgtatgtc aaaacccaaa ctgcctttat gtcaatatgc tgtaaaaatc      120
tatcagaata tatcttaatt cttaactttc attgttgtct gtggggtgtc ttgtataatt      180
attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg      240
gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc      300
aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa      360
ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg      420
caagtagaaa tgccaaatgc cagcgctccc tttccccagc tcattcttatt tgtaggcact      480
cagatttttg aatcctccag gactaacaat aaaaccacac taggtnggtt tcctaattcc      540

```

tgtgaaatga gtcagtaggn caannantta tncnctccag agagagaaca attccttgng 600
 ctacactccc tgtttcnna acccnattnc ctttctgngn ccctgganaa aggggtgccc 660
 anaatgcntg gggnnncccc ccggnctctg annaaaaacn tnttaaaaan ngccnaaagt 720
 ancctcctc nanggaagnt tcccctttta aattttnggn naaaaaannc ccttnaanta 780
 ann 783

<210> 88
 <211> 769
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(769)
 <223> n is a, g, c, or t

<400> 88
 ttggnattgn ccagcggnta acaatttcac acagnaattc cgtatttgaa atttggggac 60
 aaacaaacat aactctttct ctttccttga agggttaatg ctccaaccag cctcagattg 120
 gttcgcttga atcttaaaat tacttttctg gtcacgcgcg ccgaaggctt aagcatttgt 180
 gaaatgtctt ttttcccccc cccacccct tgatgctgtt ctctttgggc tgtcttaatt 240
 acacaggggt tgagaaacca aattaaaatt aggcgtgtct ggtcaacagt gatcacgttg 300
 catgctttta gctttgcttg ttgaagttgc ttctcctccc tgagtggctt tcctcctttt 360
 tttttttttt tttttatttt aaaaaggaaa tatcataagc tctttcagaa atactcacag 420
 gaagtgaagt tccgtatgct ggttactcac cagcaactga gtgttggcag gtggagaatg 480
 ctaccgcagc cgccagaca gatctgcaga ctggcccat tgcagangat tagacacagg 540
 gtgcgtggat catanggggt tttgtacaga aggcagtttt aagangaaan tgggcactgc 600
 atgtcatctc nanggggngg tgattcangg ancanggctg ggggtnaaaa gcacctggct 660
 gccattnngg agntcctgct aatttttaaa nggcagggtg gttttaaaaa aaaagctccc 720
 cccccccaa aaannnttt tttggaggna naacttcaa aangaanga 769

<210> 89
 <211> 754
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(754)
 <223> n is a, g, c, or t.

<400> 89
cagcttgcca acctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt 60
gtatgtatgt caaaaccaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat 120
atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca 180
tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg 240
ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag 300
tgaaatcaga aattgctgtc atacatactc acctgtgaat ggctgtacaa aggatcccaa 360
gcgaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa 420
atgccaaatg ccagcgtcc ctttccccag ctcatcttat ttgtaggcac tcagattttg 480
gaatcctcca ggactaacia taaaaaccac actaggttgt tttcctaatt cctgtgaaat 540
gagtcagtag gtcaacaac ttatccactc cagagagaga acaattcctt gagctacact 600
ccctgtttnc agtaacccta ttccctctct gtgtccctgg ataaagtgtc gcnacaatgc 660
atgggggagnc caccgggttc tgaatgagac aatcgtaaan atngccaaaa nttagctgcc 720
ntcangggaa anttncntt tgaaatttaa gnaa 754

<210> 90
<211> 866
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c, or t

<400> 90
tnggggaacc ctgnccagna ccttttttac tcatatccgg atcctgacct acattcagtg 60
ttctagattg aaatcacaga ttttgatag agaaaaaaaa atattctctg caatctaata 120
aaaccaactt tttttttttt tttttttttt tttagacag agtcttgctc catggcccag 180
gctagagtgc agtagcacga tctcggttg ctgcaacctc tgcctgtngg gttcaaccga 240
ttctcctgcc tcctgtctcc tgccccagcc tntcaagtag cagggattac aggcatgtgc 300
catgatgcc agctagtttt ttgtattttt agtagagatg gggctctgcc atgttgccca 360
ggctggactt gaactcctga cctcaggtga tcaggccatc ttggcctccc aaagtgttg 420
gattacaggc gtgagccatc ctgcctggcc aaaaccagca tattttatgg ataggaaatt 480
gaggcttaga tggggggaga aaaacattac acagattaaa ccacagctaa tgtcaagtgg 540
tgaccaaagg cgaatctttt attgcaggct gtgggttttt ccatgtggct ggtggtacac 600

| | |
|--|-----|
| tgcaccaagc agcacacaca ctaggccagt ttcctttgca gaccagttg caatcccatc | 660 |
| tntaanccag gatactatta ggtctcnaca ncctatggna ttttaggggtg ctcanagttt | 720 |
| aggggtgggaa aaggggacta anctncttgg nttaaggtnt ntccactggg ccctcncttt | 780 |
| nggnccnggg antttnatgc ccaaaancgg tngggccttt ttgggggnan aannccaanc | 840 |
| cnngggaaaa aaacnttttt gttang | 866 |

<210> 91
 <211> 783
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(783)
 <223> n is a, g, c, or t

| | |
|--|-----|
| <400> 91 | |
| tgggnntgnc cagcggnntaa cantttcaca cagaattccg tatttgaaat ttggggacaa | 60 |
| acaaacataa ctctttctct ttccttgaag ggtaaatgct ccaaccagcc tcagattggt | 120 |
| tcgcttgaat cttaaaatta cttttctggt cagcgcgcc gaaggtctaa gcatttgtga | 180 |
| aatgtctttt tcccccccc ccaccccttg atgctgttct ctttgggctg tcttaattac | 240 |
| acaggggttg agaaacaaa ttaaatttag gcgtgtctgg tcaacagtga tcacgttgca | 300 |
| tgcttttagc tttgcttgtt gaagttgctt ctccctccctg agtggcttct ctctttttt | 360 |
| ttttttttt tttattttaa aaaggaaata tcataagctc tttcagaaat actcacagga | 420 |
| agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaatgct | 480 |
| accgcagccg ccagacaga tctgcagact ggccccattg cagaggatta gacacagggt | 540 |
| gcgtggatca tanggtttt gtacagaagg cagttttaag aggaaattgg tcaactgcatg | 600 |
| tcattctgag ggggtgtgat tcaaggagca gggctnnggg gtcanaangc acntggctgc | 660 |
| catctcgggg gttcctgctc acttntnaaa gggcaggctg gcttntaaaa anaaatgctn | 720 |
| ccttcacccc caaanaggga ttttttttgc agngaataac ttccccaaaa tgaatngccc | 780 |
| cna | 783 |

<210> 92
 <211> 775
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(775)

<223> n is a, g, c, or t

<400> 92

```

ttggggaanc agcttgccaa anctacaggt ggggtctttc aaaatattgc gttacaaata      60
tcattttggt gtatgtatgt caaaacccaa actgccttta tgtcaatatg ctgtaaaaat      120
ctatcagaat atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat      180
tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag      240
ggggaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag      300
caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa      360
aggatcccaa gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag      420
gcaagtagaa atgccaaatg ccagcgctcc ctttccccag ctcatcttat ttgtaggcac      480
tcagattttg gaatcctcca ggactaacia taaaaaccac actagggttgt tttcctaatt      540
cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acaattcctt      600
gagctacact ccctgtttcc agtaacccta ttccctctct gtgtccctgg ataaagtgtc      660
gccaanaatg catggagagn cccccgggtt ttgaatgana cccatcgtaa agatngccaa      720
aagntagctg ccttcaaggg aagttncnt ttganattta gnagaaaaag tccnt          775

```

<210> 93

<211> 837

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(837)

<223> n is a, g, c, or t

<400> 93

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atcatttttg tgtatgtatg tcaaaaccaa aactgccttt atgtcaatat gctgtaaaaa      120
tctatcagaa tatatcttaa ttcttaactt tcattgttgt ctgtgggttg tcttgataa      180
ttattatcac atctacagta ttttctgtag gtaaataatga aatgtattat aaatgtacca      240
gggggaaaat gccctttaat aagcctttcc ctagacaaag caccatttag gcgtttagaa      300
gcaagaacta gtgaaatcag aaattgctgt catacactac cacctgtgaa tggtcgtaca      360
aaggatccca agcgcaggac ttgtcctgga agcagaggat cggattccac caggaaaaga      420
ggcaagtaga aatgccaaat gccagcgtc cctttnccca gctcatctta tttgtaggca      480
ctcagatttt ggaatcctcc aggactaaca ntaaaacccc actagggggn ttncnnantc      540
ctgngaaatg agtcagtagg ncaaacannt ttncnctcca nanannnaan antcctggn      600

```

```

ntacnetccc tgnatcagna acccnattec ctncntgggn ccnggnaaaa gggcgnccca      660
aatggngggg ngccccccgg nttntnanga aacccatnnt aaaattnccc aaaantttnc      720
nccccnnann gaaannnncc nttttaaaatt ttnggananaa aaanccccnt naaaaaaana      780
ngggggcggn tttntttttn aaagaaanaa anattttttt ttnggggagg ggtnnt      837

```

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<210> 94
<211> 837
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(837)
<223> n is a, g, c, or t

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```

<400> 94
ttgggnacc ctgncagncc anttttactc atatcggatc ctgacctaca ttcagtgttc      60
tagattgaaa tcacagattt tggatagaga aaaaaaata ttctctgcaa tctaataaaa      120
ccaacttttt tttttttttt tttttttttt gagacagagt cttgctccat ggcccaggct      180
agagtgcagt agcacgatct cggcttgctg caacctctgc ctgtcgggtt caaccgattc      240
tcctgcctcc tgtctcctgc cccagcctct caagtagcag ggattacagg catgtgccat      300
gatgcccagc tagttttttg tatttttagt agagatgggg tcttgccatg ttgcccaggc      360
tggaacttgaa ctcttgacct caggtgatca ggccatcttg gcctcccaa gtgttgggat      420
tacaggcgtg agccatcctg cctggccaaa accagcatat tttatggata ggaaattgag      480
gcttagatgg ggggggaaaa ancnttnccc aaattaancc acagcttatg tnaagtgtg      540

gncccaggcg gnccnnnctt tggncnttt tcttttgaa ccngntgca atcccccttt      660
taanccggga atcttttggg tttcncnccc cttgggnatt nngggggccc caanttnngn      720
nggggnaagg gnaaaaaacc cctttggntn agggntttaa aangggncce ccctttggnc      780
cnggggnnttt tntnccnaan ngggnggggt ttttbtgngg annaacnncn acnnggn      837

```

```

<210> 95
<211> 812
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(812)
<223> n is a, g, c, or t

```

<400> 95
 ttgggggttg gagcggntaa cantttcaca cagaattccg tatttgaaat ttggggacaa 60
 acaaacataa ctctttctct ttccttgaag ggttaatgct ccaaccagcc tcagattggt 120
 tcgcttgaat cttaaaatta cttttctggt cacgcgcgcc gaaggctctaa gcatttgtga 180
 acaggggttg agaaaccaa tttaaattag gcgtgtctgg tcaacagtga tcacgttgca 300
 tgcttttagc tttgcttggt gaagttgctt ctctccctg agtggtttc ctctttttt 360
 tttttttttt tttattttaa aaaggaaata tcataagctc tttcagaaat actcacagga 420
 agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaatgct 480
 accgcagccg cccagacaga tctgcagact ggccccattg cagaggatta gacacaggg 540
 gcgtggatca tagggttttt gtacagaagg cagttttaag angaaattgg tcaactgcatg 600
 tcatctcgag ggggtggtgat tcanggagca gggctggggg tcanaangca cgtggctgca 660
 tctcgnggt nctgctcant tttaaaggn ngctggnntt aaaaataang ntncctcacc 720
 ccaaaangaa ttttttcag gnaaannttc naaaaganna cccnantttt tgnnaaaacn 780
 tgggaaancc ccntttnaan ggnggnntta an 812

<210> 96
 <211> 805
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(805)
 <223> n is a, g, c, or t

<400> 96
 ttgggggancn gcttgccaan tctacaggtg gggctcttca aaatattgcg ttacaaatat 60
 cattttggtg tatgtatgtc aaaacaaaa ctgcctttat gtcaatatgc tgtaaaaatc 120
 tatcagaata tatcttaatt cttaactttc attgttgtct gtgggttgct ttgtataatt 180
 attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg 240
 gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc 300
 aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa 360
 ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg 420
 caagtagaaa tgccaaatgc cagcgtctcc tttcccagc tcactttatt tgtaggcact 480
 cagattttgg aatcctccag gactaacaat aaaaaccaca ctaggttggt ttcctaattc 540
 ctgtgaaatg agtcagtagg tcaanaact tatccactcc agagagngaa caattccttg 600

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PCT/US2003/037143

agctacactc cctgtttcag naaccttatt ccctctctgg gtccctggat aaagggctgc 660
cacaatgcat ggggagcccc cnggntnttg atggnaacac tcntaaaaat tgccaaaagn 720
tnnctgcctn aangaaaant nccctttnaa tttttggana aaaaanccct tnaanaaacn 780
ggggggcggt ttttcnttaa agaaa 805

<210> 97
<211> 854
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(854)
<223> n is a, g, c, or t

<400> 97
ttggggaacn ngcttgccaa ntctacaggt ggggtctttc aaaatattgc gttacaaata 60
tcatttttgg gtatgtatgt caaaaccaa actgccttta tgtcaatatg ctgtaaaaaat 120
ctatcagaat atatcttaat tcttaacttt cattgttgc tgtgggttgt cttgtataat 180
tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag 240
ggggaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag 300
caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa 360
aggatcccaa gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag 420
gcaagtagaa atgccaaatg ccagcgctcc ctttccccag ctcatcttat ttgtaggcac 480
tcagattttg gaatcctcca ggactaaca taaaaaccac actagggtgn tttcctaatt 540
cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acatttcctt 600
gagctacact ncctgnttcc agtaacccta ttccctctct gggccctgg ataaagggct 660
gccnacaatg catngggggg ccccccgggt tntgaangaa aanntnntt aaaaatngcc 720
aaaanntaac tnccctcaan ggnnannnnc cccttttnaa ntttttgggn aaaaaaanc 780
cccntnaaaa aananagggg gggnggnttt ttttttnnaa aanaanaann aanntttttt 840
tttggggnan annt 854

<210> 98
<211> 912
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(912)

<223> n is a, g, c, or t

<400> 98

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ttttgttggt ggggnntgna gcgncggctn aacttttttg cacacagaaa ntcacaggaa      60
cacaggagtc agtttcttca gcaangtctt gcttgccng ttntgaacgg taggatnttg      120
tcgctatatt tgnacacatg agggacctnt gtggagcttc caaatagtgc gctnggcgca      180
atatnnacaa ganacagccc ttagcgantg gcttggtgnt gggngagatg ntgctctgtg      240
ngatgaattn acanatcaca gagttttttn ttgnntgct tgtttcctgt tntnaacgg      300
ggatttgtgn ttttggaaca tgggatntct atgggctnan agangtccta tgtnggaata      360
nggcaatgta ctgcctttna naactggaat gangctnggt gagaanctgc tctgtgttct      420
gtganttcog tactntgaaa ttgggggacn aacaaacata nctctttttt cttttccttg      480
aaggngtaat tgctccaacc ccgccncaga ttgggntngc ttgaatctta naattntctt      540
tctggtcccg cccgccgang gntnagcttt tngnnaaatg gtnttttttc cccccccca      600
ccccttggtg gngggtnntt ttgggcttgg nnttnanntn cccccggggg nntngnnnna      660
ccnatttttn attttggggn nttttgggnc ncanggggtc cnnnnnnnnn gnetntnann      720
cttggttgn nngaangntg nttntcccc cccggggggg tccccccnt ttttttttt      780
ttnttttttt ttttnagggg antttntng tcttttttna annncncgg gntggggggg      840
tcnntttttt gtttttnncn nnnnttgggn nggggggggg gganntttct ctnnnncccc      900
cnnnttttn gc                                                    912

```

<210> 99

<211> 807

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(807)

<223> n is a, g, c, or t

<400> 99

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gtatgtatgt caaaacaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat      120
atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca      180
tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg      240
ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag      300
tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa      360
gcgcaggact tgcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa      420

```

atgccaaatg ccagcgctcc ctttnccag ctcatttat ttgtaggcac tcagattttg 480
 gaatcctcca ggactaacan taaaacccca ctaggttgnt ttcctaattc ctgtgaaatg 540
 agtcagtagg tcaaanannt ttncnctcca ganaggaaca attccttgag ctanctccct 600
 gtttcaggaa ccctattccc ttntgggncc ctggaaaang gctgccacan tgctgggaag 660
 cccccgggtt tnaangnaaa aatcnnaaaa ttgccaaaan tancnncccn agggngngtn 720
 cccttanant ttntggaaaa aancnccnta aaaaancngg gngcgnnttt tnttaaaana 780
 aaanaaattt ttnttngggn gnttttn 807

<210> 100
 <211> 814
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(614)
 <223> n is a, g, c, or t

<220>
 <221> misc_feature
 <222> (1)..(814)
 <223> n is a, g, c, or t

<400> 100
 ttggnattgn ccagcggnnta acaatttcac acagnaattc caggcacagt tggtctgtaa 60
 ctagaatagt aagtggcttc ctaggctctg tcaactcctaa actgtagggg gcttccagcc 120
 tcggagatta cggaagtagt acttttcatt agcaagctca agaagaagtg tcaaaatag 180
 atgacacttt cctagtcgct ctgcaaaaac ccaaaaaacc agaaggggtg tcactctagac 240
 actcctaagt ctatgcaggc gtcagcctgc cctcacccaa caccagccag cagcgtgcac 300
 cattcaacca tatcttaact tgccccttac aaattgacac ttactactaac aagccctttg 360
 atctcatttg tttaaaatga cagatataca accctcacgg gggttccac tcaaggcctt 420
 ncagcctnng ncctgcccc gncaccccc aaacctacac acgtgttagc ccgacaccgg 480
 cccaccggg tcccacgtgc acctggtcta acacactncc cacgtgtggg cgccccacgg 540
 gctttctnan gtagctgang gnccccccat gacccccgt tntccaaan aaaaaaacgg 600
 gaaggacaag ggcccttttc nccngngncc caacctnng gggggnggt ccaaccctt 660
 tnttnntat aaaccccaaa aaananaaag ggccggggn ccncccccc ccttnaaaaa 720
 nccgncccc cnttttnccc ccnnaaaaaa nggggggaaa aaaaaattt aaaaaannc 780
 nttttttnt ttttncccc ccnncatnta nata 814

<210> 101

<211> 756
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(756)
 <223> n is a, g, c, or t

<400> 101

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gcacttcccc gacaatctac aaccccatcc aaaggggtca gaaactggta ataaaatacc 180
agctatgagc ctntccttcc cctcaagaga tctatcaatt cggcctcacc ttcccacctc 240
tagcctgcgg gaacaaacat cccaggatcc cgggcgggtt cgattgacgt tacttccggg 300
aaaagtaacc ttgcttcggc ggttgccggc ctgaaaagct ctgcgcacat ttctctccgc 360
nagatctgct tgctcactgt agcgatgaca tcctcctcct cctccccgcc gcctttcggc 420
aatcttcgcc agtcccagcc cggaccaatc tgtactcaga tggcatggat caggggtctc 480
cctcgaaccc cggttcgcac ggggcgtcag gtggcagcgg cggggtgcga gctgcgcgag 540
gccnacngca gcggcactgc ggggtggcng gggcaggcca caagcantga ntgtnggccg 600
ggccgggggn aacccacccg ngtagcggct cnantgnttc tggcctggct ttngngccct 660
tttctcccc ccncanggt tcccggnnc ctgttncgnt tcttttaann ggggaaaggg 720
gcccccccc ccccnngcca angcccnnn acnnnt 756

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<210> 102
 <211> 804
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(804)
 <223> n is a, g, c, or t

<400> 102

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tgggntgncc agcggntaac antttcacac agaattccaa ttatggggaa caagacatct 60
gaattggcta aaactccttg cagcagcaaa aaggaaaagc aaaacaaaac catacatgtg 120
gtttctgtct ttgcttctg tcttttcttc caccttactc ctcttcccc ttccccttcc 180
ccttccccct ccccatcttt gtacacaaaa aaaaatctag agaagccttc tattaacctg 240
aacccttaa agaagtcaga acaaaggcac cacttgccgc tttttgggat gtcgtgtttt 300
ctttatggag ttttcaagag taatgggcag atgcttttag gtctacagtt ctgctttcct 360

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```
gtattgcact acctgattct ttgacttttg gagataccag aaattacctt gtaccatgag 420
aggatttggc tttggcatgt gtaatggcag atgagagcta caaagttaag agtggctgaa 480
gatggtttac atgaagtggg cttaggtggg ttagctgagc tcccaggaag ttgttgctta 540
ggatcccaat tctagttcag aggtgcattc ctattattat tatcattact attgggtggtg 600
ntgntattat tttgagacag agtcttgctc tgttaccoca ggctggagtc ctctggcacc 660
attacgggtn actggagcct naanttccag gctncagaga tcctcctttt annttcnnag 720
tagtgggacn canangnngg nccccccaa cnnannnatt tttgnncttt tгнаanaann 780
gggtttgntt tttngncnnn ntgn 804
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<210> 103
 <211> 795
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(795)
 <223> n is a, g, c, or t

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<400> 103
ggnattgncn agcggntaac aatttcacac agnaattctg gagttagggt gtctgggcta 60
ttcaattagt ttctatgtgt ctgacacatg gcagaaactt attaaatgct tgaatgaata 120
cataaagcaa gatgacagtt tcagaatgna ccaggtaatt caaagtactg aatccatatt 180
aaatttattt tagtctacac agaagtgaag taactactaa atctgggcat ttaccagggtg 240
atggcaagta ttcatttcca tcatccagcc cggtacctgg cacatagtta ctgccctatg 300
taaagtctta tcacagcaat caatcaatga aatgtttttc tcatagagtt cgggtgaataa 360
ctcacgacag catactcaca gaggattcaa agagtatttg acttgatat attgttttaa 420
acagttggaa cctgataatg cagttttcta aaatacagtg aaagggttg tcctaaaggg 480
catgtcagga tatgtgtgag aaaggatgaa cttgtcctgt gaagacaacc ttgcattagc 540
tctagcagaa tgagccattg cctacctggg ctggggaagg cggcacctca gtatctccct 600
cacctgctcc ctggcacttt aaatccctct gtgaagangt cagttgtaat tttcagtaag 660
attgaagggt tcaaagcact gaccctggg ggggaatggat tngcttaagt tggctctgaa 720
ngaagnggct gggatnngct ntctganaaa cccgggattg tgaggnaatg gagacngccg 780
ggagggttna anaaa 795
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<210> 104
 <211> 641
 <212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(641)

<223> n is a, g, c, or t

<400> 104

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tgggggnacc cagcggntaa cattttcaca cagaaatctc attcaatgaa ctgttatggg      60
gtctcacatt gtaccaggca ctggggattc agcttccagt tcatagtctg catgcaaacc      120
gacatgcagg tagacatgca gacagaaaat cggaacgcaa cacggtaagt gctatgctag      180
agaatgagaa ggactgtcag taatcacaac cacctttcac tgggttcctt cagtgtgcca      240
ggctcgtgta cattattttg tttagtgtc acaattgtat ggactgtgta ctatcatttg      300
ccagattata tggatgaaga aactagactg aggggggttaa ataactcgtc caagatcatg      360
cagacaaaaa accacagaga ttattttcca atacaaactc tctggctgta cagctcaagt      420
tcttaaacac tgggccaacc agtctgaatc tgagaggagg cattctaagg cttacaggta      480
agtgggaatt gaaaggggtg agggaagcct tctggaggag atgccattac actgaatgtt      540
gaatgagtag gagttagcta tctccagagg ggtagtggct gtgaaggggc gaggggtana      600
gggtgggaag gggatgatgg aagggtgtag agtggnnaca g                          641

```

<210> 105

<211> 757

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(757)

<223> n is a, g, c, or t

<400> 105

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cngncttgcc aacctacagg tgggggtcttt caagatctgc tgacagtgaa gctaaatctg      60
gcggaagcaa aggattcact ttctcataat ggattaactc atcctatttg cctcttaaac      120
aatgggtatt ttaaagacag aagttgaagg aagtccaagt atccaatttt aaggatgcct      180
attagagcag ttataagaga gtgtctctct ttctctctct tctttctttc tcttggtagg      240
agtatgcagg aggtcattta aaagccagat agtgatacaa atcacaatgc agaaaaacat      300
ccccgtggac tcctccctgt cctatgtttg acattcttaa aatctatgtc ccaggctctg      360
aaatctttta ataacttacc atgttctttg gcctgccctg ggaaatctat ttcagtacca      420
gagctatgct ggttacacac cttttctgac tcatgttccc aagtgatttt attccagata      480
cgatttgggg acagttacgt gtactgttct gatattctcc taaaaggaaa ttatttttgg      540

```

aagtaaagtc actgataaaa tcanetcagg aaaatgcact ttgtaaatat taaaatataa 600
 actttttnaa ggncttgctg gaaaanacta attgattttc ctgggnagca gttccatnga 660
 acancgatng atcttttaggg ggnagtgaan ggcccnatt tgaaaaangg gggcgggaaa 720
 ngttcaaata ntttttccaa angggnnccct anntnnt 757

<210> 106
 <211> 640
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(640)
 <223> n is a, g, c, or t

<400> 106
 ttgggggnanc gagcggntaa cattttcaca cagaaattca ttcaatgaac tgttatgggg 60
 tctcacattg taccaggcac tggggattca gcttccagtt catagtctgc atgcaaaccg 120
 acatgcagggt agacatgcag acagaaaatc ggaacgcaac acggtaagtg ctatgctaga 180
 gaatgagaag gactgtcagt aatcacaacc acctttcact gggttccttc agtgtgccag 240
 gctcgtgtac attattttgt ttagtgctca caattgtatg gactgtgtac tatcatttgc 300
 cagattatat ggatgaagaa actagactga ggggggttaa taactcgtcc aagatcatgc 360
 agacaaaaaa ccacagagat tatttttccaa tacaaactct ctggctgtac agctcaagtt 420
 cttaaactact gggccaacca gtctgaatct gagaggaggc attctaaggc ttacaggtaa 480
 gtgggaattg aaagggttga gggaagcctt ctggaggaga tgccattaca ctgaatgttg 540
 aatgagtagg agttagctat ctccanaggg gtagtggctg tgaangggcn aggggtaaag 600
 ggtgggaagg ggatnatgga aggggttnaa tngggnncnng 640

<210> 107
 <211> 818
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(818)
 <223> n is a, g, c, or t

<400> 107
 ttggggacca gcttgccaat tctacagggt ggggtctttca agatctgctg acagtgaagc 60
 taaatctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc 120

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| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|-----|
| tcttaaaciaa | tgggtat | aaagacagaa | gttgaaggaa | gtccaagtat | ccaattttaa | 180 |
| ggatgcctat | tagagcagtt | ataagagagt | gtctctcttt | ctctctcttc | tttctttctc | 240 |
| ttggtaggag | tatgcaggag | gtcatttaaa | agccagatag | tgatacaaat | cacaatgcag | 300 |
| aaaaacatcc | ccgtggactc | ctccctgtcc | tatgtttgac | attcttaaaa | tctatgtccc | 360 |
| aggtcttgaa | atctttaaat | aatctaccat | gttctttggc | ctgccctggg | aaatctat | 420 |
| cagtaccaga | gctatgctgg | ttacacacct | tttctgactc | atgttcccaa | gtgattttat | 480 |
| tccagatacg | atttggggac | agttacgtgt | actgttctga | tatcttccta | aaaggaaatt | 540 |
| attttggaag | taaagtcact | gataaaatca | actcaggaaa | atgcactttg | taaatattaa | 600 |
| aataataaaca | ttattaaagg | ccatgctgta | aaaataactaa | ttgattttcc | tgggtagcag | 660 |
| ttacaataga | acancgatng | atctctaagg | ggagagtga | aggacctcan | tttganaaac | 720 |
| gtgaggcagg | aaaagnntca | aatnattatt | tncaanaggg | ntccctaagt | tgttncttaa | 780 |
| anaaaatttt | tttctntnaaa | aaaaaacnnt | aanggccca | | | 818 |

<210> 108
 <211> 608
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(608)
 <223> n is a, g, c, or t

| | |
|-------------|--|
| <400> 108 | |
| ttgggacct | gtcagaccan ttttactcat atcggatccc ctgaggctcg gagatcaaga 60 |
| ccaccctggc | caacatggtg aaaccctgtc tctactaaaa tacaaaaatt agccaggcgt 120 |
| ggtaggcaggc | gcctgtaatc ccagctactc aaaggctgag gcaggagaat cgcttgaacc 180 |
| taggaggcag | aggtggaagt gagccgagat cataccactg cactccagcc tgggcatcag 240 |
| agccagactc | gtcgcacaaa aaaaaaaaaa aaaaaaaaaa attagctacc tctcccatcc 300 |
| anaaatgaga | gtcagaggct ctgacttccc gggctcaatt tatcctcccg cctcagcctc 360 |
| ttgaggaact | gggactacag acgtgcacta tcacacttgg ctaatttttt tgagatgatg 420 |
| tcttgctctg | tgcccaggct ggagtacagt gacacaatct cagctcactg caacctccgc 480 |
| ctnctgggtt | caaccgattc tnttgcttca gcctccaag tagctgggat tacaggcgtg 540 |
| ccccacaacg | tccagntatt tttgtatttn aagnagagac nggggnnncc cctgttggnc 600 |
| ngggngggg | 608 |

<210> 109

<211> 516
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(516)
<223> n is a, g, c, or t

<400> 109
nggganccctg nccagnacct ttttactgca tatcggatcc tgagaagctc ctgattttcc 60
ctcaagccta aggcaaagta gtattcagaa cctcctatcc cactgactcc gagagcctgt 120
cctccgatat ctccaagaga gcctatcctc cgataggagg ggaagcccct ccaacctgca 180
ggtatcctcc ccagactcac catttctccc accccacact ggtggcttcc aaactttccc 240
tctcataaca aggcgcctg tcaccagac tgcttcctc ggcttgagga ggaggggaag 300
gcgcacgaag taggaaggaa cttggggaga gggcgggagg aggggtgggcg aagcactgag 360
gggagggcgg tgaagaaggc agaagtcagg cagtgaagg gagaaagcggc gggggcagggt 420
gagggcgggg gagtggggat ggggccgggg aaaggggccg agaggacgcg gagggggcag 480
aggtagggna caggagggga ggggaggggg agggcc 516

<210> 110
<211> 802
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(802)
<223> n is a, g, c, or t

<400> 110
tnggggaacc tgccagacct tttttactca tatcggatcc ttattgcctg gctatttcag 60
cctgggaggg gtttggtggt aatatccctg gggaggcagg ctctcagggc taaaatagtg 120
ggagaaaaga ttaaaccttt aggaaactgg tacacatcag cgctaagtgt gactcagggg 180
gaaacaagaa ctaggacact tattactcca aaggagtgt atttggttca actcttgtat 240
tttcttatta aaacttttgc aaagtgggtt gagaagaaag tgttacttcc agtgttacac 300
cctcaacact ttttctgtg gagactccag catgttcatt atgttttctg aagccatggc 360
actgtagtac tctttcattg ttgttattat tatttaataa tataaaatga gacatttttg 420
ctccattttt cattcatatt ttgtcctaa ttacttttta aatatattct ggtgtcagggt 480
caatatttat agtctaacgt ttaagactta gactttgggt cttaggatgt tatttttgaa 540
tcagctgcgt ctggttaagg aatagatatt gaaagtgcct tgtaaattgt ccagtggcac 600

aaaagtattg tcatatcttt atgacataaa agaaaantgt tttcttctct ttagcatgga 660
aaactttaca anccatttgc tgggtgacngg ngangncctn ggggttgatg ttcattgattt 720
tggggtccct tgagggtcca aantaccntt ctaanagngg aaanttttca nnaattcatg 780
antgncctna ttnaaanann tt 802

<210> 111
<211> 851
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(851)
<223> n is a, g, c, or t

<400> 111
tacttttttt tgggggnncc aagncggnta acattttcac acagaaatct ccaagttccn 60
naggaccgca gnatectccc cagaaccctt gngaccaagt cactgtgggt ggntgtgctg 120
ggcatccctg agggccagcc actcaacttt actggctcca ggattctata gaaagggaaa 180
ggggtagaaa atctcaaaag gcttcttctt ttcaggggagg gggttccctc tcagcggtt 240
ctggaatctc taccactctc agccgacttt tgaggccatg tggctctgga acaaggcccc 300
tctgaggggc gcagatgggg caggcgcccc aggcacacag catggttggc tctgcgcccc 360
agggccaca aaagccttat tgagtcacca ccagcccccg gcagaggctg aggtggcagt 420
ggcgccgagc gcctgccacc taatgactgt cctggcacag ccagatgttc cgcagacctc 480
cggagcagcg ggaccaaggg cccgcccggg ccagccggca ccngannagg ccacttttaa 540
tttccaatta accagntttc agnntgancn aaanaggggg gcagtnggtg gnccaccccc 600
cgggcnagta ngccccggcc cnnaaaannc cttncgaagt tntaanactn ccanatntga 660
aaccnccacc nccngaatt ccnatggaa aaantggccc ccagccangg gcaagggntt 720
gggncctttc ttttcttttg aaaaggaaat tttggttntt ttnacnaagg cccccaang 780
aaccnctatt t 851

<210> 112
<211> 773
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(773)

<223> n is a, g, c, or t

<400> 112

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cagcttgcca antttacagg tgggantctt tcaagagcag taaaacgacc tatccaagga      60
aactcagcta gtaaaggcag ggacagggta tcgcaggctc tcggaactca cgagtccccg      120
ccaggcgcat ggccgctcct ttcccccggt gggcgtaggc aggccaggcc cgtcccctcc      180
cctgagcgcg ttcttgccag cccggccggc cgttttctgc ctgcgtcgct gggcgcgcg      240
gcgggcgggc agcccatctg gcggccccc cggggcgggc cggggaggcg gccagactt      300
gctggagcca ggcgcctgcc cgggggcccc cctgcccgcc tggagaacct aggtgtggcc      360
gcggcggggg tggggggtgg tgctttcctt cccgctcgct cggctcttnc tgacgcacga      420
gggcaggatg cagcctctc cgcctctctc ctgcgcctcc gcctcccgcg ccctggcccc      480
gaatcctgga gggaatccaa acgcggggcg gggaggccgg ggcaggcccc tgaggcccc      540
cccctgatag ccatttaata ccaccgcaag tcttgaccgt atttttgggg tgaccanct      600
tccctgcttg ggcaagacca gctgaactct gacctnctgg anggccgatt ttaccttgct      660
cctcagggac ccnnaaatga tcgtaggaac cngnntcact actgctgtaa gccanancg      720
ttganatatn caattattca gcggnattcaa gtcccgaag cggnntttna cna          773

```

<210> 113

<211> 807

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(807)

<223> n is a, g, c, or t

<400> 113

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ttggggttgc gagcggnata cantttcaca cagaattctt cagtgaattt cttaagccct      60
gagcatcttc tttgtattct gctttaagaa cttgtttgtt tctgtatttc atactcagt      120
gctctggcgc ttggatgcc tggcccaca gaaggccttg aatactgaat ctgaggatgg      180
ggcttgctta taaggacctt actccctgtc ttaaccagat tgtgttttaa cctttcatct      240
cactttttac ttttcattca tggatagtgt ttgtcactgt gtgtgtgtgt gtgtgtgtat      300
gaatgagtga atgaatatct ctacactct aaattctttt aaaggcagga agtactgttc      360
tcttgtttgc tattttatcc actctgcctc tactgggtct ggcacataat aaagaaagaa      420
tgaacaggac aaacacccat tctgaaagtg aacttctctg gcaattgtcg tttgtacata      480
ccagctggag catagacaat tggtttttaa tgtggtaagg gaaaaggta aaaaaagaat      540
cgtcattgac caagggttc accagatgat tttataatca ntccnaaagg gnctttnaan      600

```

aaaaaaggcc ttngagggaac aaatttnttc cnnntggaaa antgntttna aattttntn 660
 gaaaaagttt tnanaatttt tgnaaaaccc ccccccnnt gaaaacntnt aaancnngna 720
 annngnnnng ggcgggggtt naaaaaaaaa aantncccc cnnnnaannng ggnctttnaa 780
 aaannnnngn ntnctaaaaa aangggg 807

<210> 114
 <211> 836
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(836)
 <223> n is a, g, c, or t

<400> 114
 ttggggacca gcttgccaan tctacaggtg gggcttttca gtatgtgtca agagtcagaa 60
 tttaaagaag ataagaaaat taaatacact gagaacaatg catctcntga cattcaaaat 120
 atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct 180
 ataaaaagaa tatctaaaat tgctttttta tgaaagttcc tatttattct tgtttccctt 240
 accagagagc ctgctttccc cttactgatg agaacacagg gggctcctggg taaagagtcc 300
 ataanattta aaaaggagta tgccttggcc tcccatgacc ctcttacttc acaataaggc 360
 catcttttac ctggtttaga tttgcagact aggtccatta gatacgttgt cattaaatac 420
 ctatactata ccctaataat tgtaatcttg acaggtatta ttttcatttt atagacagat 480
 ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt 540
 ttaacttggtg tttgccactc tgaaactcac actggaattc gagactagtg tgcgtaacat 600
 ggcgaaaacc catctctatt tntntttttc aaaatntntt tttccaaaat ttgctggggg 660
 tgttggtgtg tgctgtant ncagcctnct tgggaggctn aanngngnga cngcttgacc 720
 ctggngnaa aggctaaatn gnctttnttn gccctggan ttaaccnngg ggaaaaangg 780
 aaccttntc aaaataaatt ttaaattaaa naangccnag gtttcccna aaaaat 836

<210> 115
 <211> 839
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(839)
 <223> n is a, g, c, or t

<400> 115

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ttgggananc gagcggntaa cattttcaca cagaantcca gtgtgagttt cagagtggca      60
aacacaagtt aaaatcatga ctttgcctctg tgatatttga agggattccg ataagtcatg      120
taattttcct agatctgtct ataaaatgaa aataatacct gtcaagatta caaatattag      180
ggtatagtat aggtatttaa tgacaacnta tctaattggac ctagtctgca aatctaaacc      240
aggtaaaaga tggccttatt gtgaagtaag agggtcattg gaggccaagg catactcctt      300
tttaaatttt atggactctt taccaggagc cccctgtgtt ctcatcagta aggggaaagc      360
aggctctctg gtaagggaaa caagaataaa taggaacttt cataaaaaag caattttaga      420
tattcttttt ataggttttg gcaaagggtg ataaaaggcc tatggaatta ctgctggttg      480
ctgcacttac atattttgaa tgtcttgaga tgcattgttc tcagtgtatt taattttctt      540
atcttcttta aattctgact cttgacacat actgaaagac cccacctgta ggtttggcaa      600
gctagctgag gatcgtttcg catgattgaa caagatggat tgcacgctgg ttctccggcc      660
gcttggtgag agaggctatt cggctatgac tgggcacaca gacantcggg tgctctgatg      720
ccgccgtgtt cggctgtcan cncagggcnc ccgntttttt tgnaanaccn nctgnccggg      780
ccctnatgaa ctgnngacaa ggcacccggg ttntnggttg ncnaaanggn gttntttgc      839

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<210> 116

<211> 815

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(815)

<223> n is a, g, c, or t

<400> 116

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tnggggacca gcttgccant tctacagggtg gggcttttca gtatgtgtca agagtcagaa      60
tttaaagaag ataagaaaat taaatacact gagaacaatg catctcaaga cattcaaaat      120
atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct      180
ataaaaagaa tatctaaaat tgctttttta tgaaagtccc tattttattct tgtttccctt      240
accagagagc ctgctttccc cttactgatg agaacacagg gggctctggg taaagagtcc      300
ataaaattta aaaaggagta tgccttggcc tcccatgacc ctcttacttc acaataaggc      360
catcttttac ctggttttaga tttgcagact aggtccatta gatacgttgt cattaaatac      420
ctatactata ccctaataat tgtaaatctg acaggattta ttttcatttt atagacagat      480
ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt      540
ttaacttggt tttgncactc tgaaactcac actggaattt tnggggaaat nntatccgnt      600

```

canaattccc ccnecatgag cgtanacccc cgaaaaaaga acaangatnt ttttggaacc 660
 nttttttttg ggggnaannng gngnngnaaa aaaaaaccnc cnntncnacg ggggtttgtt 720
 ggccgganaan aacnccacct tttttccnaa ggaaangntt tnaaaangcg aanacaaaa 780
 ntgtcntttt gnnnggccgg gttggncccn cttna 815

<210> 117
 <211> 792
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(792)
 <223> n is a, g, c, or t

<400> 117
 ttggggganc gagcggntaa cattttcaca cagaaattcc cgacctcaag tgatatatcc 60
 accttggcct ccaaaagtgc tgggattaca ggcatgagcc accgcgcccg gccccttcat 120
 gcagtttctc tcaactcctt cagaatcgag gagtctgcta ttccatcgac atctaacca 180
 ctccctctaaa ccagcctgca atcccagctg gagaactaca atccaatcag ggattaaatc 240
 taaattcctc ccatctgatc actgggatcc ctacccattc aactcccctc ctccctcaga 300
 aatgttacca atcccctaaa gcctccaatc acctgttgag ccaccagcca agcgcttact 360
 aatccctgtc tccaagctc agacactccc tgtaattgat ggacacgcag cattggggagc 420
 tttcacattg agctcttact ttgaaacttt gaataagaaa agagctgaaa aaagcagatc 480
 tccaatctc ggtgaaactg tagttaaact ccaagtagaa taccccaata aatggatang 540
 aatganaaat ctcatatggg ttatatangc antatttana aattttggaa ttataggmnt 600
 anggatncaa actnnanan tantattcca ttggnntttg gngcnccna ngntaaanaa 660
 gttnnccnct canaaggaaa nggggngggg nangggctan nccnaancc annttttggn 720
 ggnnggnnn aaantttttn ggnccaantt naaanaaann tnntnaaaaa aanggnccn 780
 tttttnaaaa aa 792

<210> 118
 <211> 838
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(838)
 <223> n is a, g, c, or t

```

<400> 118
gggnaaccga gcgntaaca ttttcacaca gaaantcgga aagtaaagcc aatcttagag      60
gctgcaggag gtttgggggc agtatctgat tcagacgctg gctaacgttt cacgatcgcg      120
ttcccttttt tcttccaact cggtaagtaa aaaggcaaga tgagaaattt acgtgctgaa      180
cttaataaat agttggtgga cgtattgcct tttttttttt ttttttggtg agggatgaca      240
catctcgtga ctacagttct tttgaggaat aacttttctg ctagttttcca aatcggcacg      300
tgaccaaagt cttttcatag gatttttagcg tcctgataaa aatcaatggg cagaatttga      360
ttgcttttta aaaaatgtgt ttgtcctttg gtctctggca ccattgtaat ggaaaatccc      420
tacattgcct gtactctcag aagctgtcca gtggagcaaa actagagata aagaaacctg      480
gaacgattca gttaggaact tttaagaagc cagccttttag ttttcccttt agaagattat      540
gcagttatca tgattgcttc tctagaactt cagtgtgtta tttggattcc taaatctaag      600
acaatgctgn ggaagtctgg ggcttttagt attttngggt ctgctgnaga aaatcctcgt      660
ttatactaca aagtttctnt tttggaactt tnggaattgg gcattttttt nnttattatt      720
ngnatgntng antnannggc aaaactnagn naaccctttt nggtttgcct cnanccggtt      780
nttaanaaaa ngggaaaaan cctnanttta aanttttttc cacccttttt tntttnt      838

```

```

<210> 119
<211> 820
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(820)
<223> n is a, g, c, or t

```

```

<400> 119
ttgggganct agcttgccaa ntctacaggt ggggtctttc agtggggggc tgtcctgtag      60
gttatagaat gtttagcagc aaaaattaaa aattaaataa caaaaataaa aataaaaaag      120
aatgttttagc agcatccctg gcctctaccc actagatgtc agcagcacct cccttgcccc      180
cagggtgtgaa ccaaaaatgc ctgcagacat tgccaaatat ctctaggag gacaaaattg      240
tcctctcttc cacttgagaa ctattactct aaaattaccc agatctgctt tgaatccccg      300
ctccacccca tcacaacctg ggtcatcttg gaaaacagac tgaaccttcc tatgcccccc      360
gcaaattcct caactgtaac atggagctct tgctgaagaa atgctatgaa aattaaatga      420
aatgatgtac gtacaggatt tacacgcaca gaatattcac cgcgccagag tgagtgtcga      480
ataaatggtc agaaatgagg ggaggctaaa aaaaaataat ttcgagaact caaaaatctt      540

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PCT/US2003/037143

```
atcttttaggc ctccagagta ctgtagtcta gacagaagaa atgggttgaga tagaancaaa 600
agagatgaga gaggttgga aagaagtgat agaactaagg tattattccc cttatctctt 660
aagaaccgga cttggagtca aagccaatag aggggtctact tagttttgnc tattactcta 720
ctttcaaata taacgaaaat tgcccaaacc caaagtnctc aaaaaaaact ttnnnttnan 780
cggggatttc tncncggncn aaaatctaan nccccnctnc 820
```

<210> 120
<211> 797
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(797)
<223> n is a, g, c, or t

```
<400> 120
ttgggggtgc gagcggntaa cantttcaca cagnaattca gctgatgaat gcagatatga 60
accgatgggt caagagctgt agacatacat acctagttta ccacactgat cttcttagta 120
taaaaaaaca agcgttacta agaaacatct actttcagca aatggacatg accagaatga 180
tacatagaat gatgcaagaa atttcactct accattcatt ttaatcttta cagtaacagg 240
atgattgcta tctcaatctg tcattttacc tttttttttt ttttcagaag ttaaagtgt 300
tccatacaag ttcaacttaa cattgttaag tgcaaagtta acagtgtaca ctttggagat 360
accttttttag gtagaaaatg attttttggt ttctaataag ttttcccaag taatattaaa 420
gaagggttaa tatgtcattt acttgagaa aacagaaaac catgagaaaag tttgggaaaa 480
tgctatatat cagagcttaa tatattgaaa cagtaagtaa gacaggaatt ggctaccttt 540
taagaacggt tacaaaaata caaactgann ggaatgcttt tggcaatnaa aatntgacnt 600
gaaacattca atggcnnaac attcaanaan gnttnagana tcnttncctt tancatccaa 660
natngttttg ncgncntctc aaaaaantgt ntnttttaaa aaanttaggg ntaaaanttt 720
ctggnagntt nattaanctt tttttgnncc ctnaaathtt nccnaaagt tcnttnanca 780
aaaaaaaatn cttttttt 797
```

<210> 121
<211> 828
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(828)

<223> n is a, g, c, or t

<400> 121

```

ttgggggancn gcttgccaan tntacaggtg ggggtctttca ccttcttgcc agaaacataa      60
aatgcgatgg agctacggcg accgctgccg agacaaaatg gcgccgagaa cctgggttag      120
cgcaggcgcc ttggaaagac cctgccccgc ccccgctgcaa gcccctggct gcaattctgg      180
gttccgtttc catgggacac tccgccgcca atcctcgtgc cgaactgctc ttcctgacct      240
ctcaattcac caatcagtgc ccagtcaagc acatccggag tcgtctctac caatcatttc      300
tcaagacttg cttactcaat aaccaactct ccaataacgt tgggtcttcgg aaaaagccaa      360
tcataagtgg aagatgtcct acctgctgtt ttctgcacca atccatgaag ttctagagct      420
acatccaatg aggacggcag gtagcgaggt cctatccgaa gctcttcggc gtcataaaca      480
gccaatagga gtctgttag aagcgagtct gctcaacagc ttgttatttg gtggattgtg      540
gcagtaaadc ggggcgagtg gggaaccggg cgcaggaact gcagccgcgg ttgggagtgg      600

cgcacttnac ccgcanttgg taggtggggg agaggggaat cnggggggatn ctgaatggac      720
aaancggnan cggcagcaan tgntgntgcc cgggtncctg tgcaantnga aacntttggn      780
gtggggaang ggattctagg caanggnccc gcnanccna aaaaaggc      828

```

<210> 122

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(842)

<223> n is a, g, c, or t

<400> 122

```

ttggggganc tagcttgcca antctacagg tggggtcttt caccttcttg ccagaaacat      60
aaaatgcgat ggagctacgg cgaccgctgc cgagacaaaa tggcgccgag aacctggttt      120
agcgcaggcg ccttggaag accctgcccc gccccctgac aagcccctgg ctgcaattct      180
gggttccgtt tccatgggac actccgccgc caatcctcgt gccgaactgc tcttctgac      240
ccctcaattc accaatcagt gccagtcaa gcacatccgg agtcgtctct accaatcatt      300
tctcaagact tgcttactca ataaccaact ctccaataac gttggtcttc ggaaaaagcc      360
aatcataagt ggaagatgtc ctacctgtg tttttcgac caatccatga agtttcagag      420
ctacatccaa tgaggacggc aggtagcgag gtcctatccg aagctcttcg gcgtcatgaa      480
cagccaatag gagttcgtgt agaagcgagt ctgctcaaca gcttggtatt tgggtggattg      540
tggcagtaaa tcggggcgag tggggaaccg ggcgcaggaa ctgcagccgc ggttgggagt      600

```

ggtgctgccc ggacgggggc cccacggagg tcagagggga ggaggactct ggagctgaca 660
gcgcgcactt caccgcagct tggtaggtgg gggagagggg aatcgggggn annctgaatg 720
gacaaancgg cacgggnagc aantgntgnt gcccnnggggt cccgngcaa ttggaanctt 780
ttggaggtgg gggnanggna ttctagccaa ngggcccnnc nagcccaaaa aaangggnc 840
nc 842

<210> 123
<211> 815
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(815)
<223> n is a, g, c, or t

<400> 123
ttgggnaacc gagcggntaa cnttttcaca cagaaantcc caggctccat gcctgaatag 60
ctgggactac aggcacacag aatcatgccc atctaccttt ttattttttg tagagaagag 120
gtctcactat gatgcccagg ttggtctcaa acacctgtac tcaagagatc tccccacctt 180
ggcctoccaa agtgccagct ttacaaatgt gagccactgt ggggtggccat gaactcttcc 240
aatgaccctt tttcaaaaaa atatttcaac tattcaatgt gagccaagga tgtgccagac 300
atttgctaga tgctatgaat aaaatatgac aaagattcag tctttgtccc catggacttt 360
atagtctagt agtagatgag actcataagt aatatctagc caaaaataaa aattactgta 420
ttatgggaga ataagaatat ggtactaatt tcttcagtgc caatgtatat cttttcatgt 480
tcttgttcct tggattctca caacaattga tgaaaaatgt aacctggat ttgagtttgt 540
agtcttattt tccaacatga tgaagttgtt attaagttg agatgatcaa gggagactca 600
ggaagcagtg ggtaacctca gctaaaagca aacagatagt atattggaag atgaggtaaa 660
caaagagagc aaagctttat gaatctgggc taaaantcag ctataagtnt tcgcanatcc 720
angagaactt tncaacagnt tncaattgaa anccttnag tttttaaann cctntttttt 780
caaantgncn aaannnttaa caggnttgna atncc 815

<210> 124
<211> 823
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature

<222> (1)..(823)

<223> n is a, g, c, or t

<400> 124

```

ggnnnttgcca gcggnntaaca atttcacaca gaattcaaac tccagcttta ctaccctgtg      60
accttgggca  ggtcacttca  catttctcag  gctggtttcc  agtctggctg  cctttgggga      120
ggggacctgg  gtttgcagga  agaaaacttc  cttacactga  ataattattg  ccttggttaga      180
aatttttttac catgtgcaca tattactttt cctaaatatt tgcacccaat ttaattgatt      240
taattgggga  aaaatgaaca  taggaaaaat  aatgacctct  tcctcagggt  tattaanaag      300
tttcaaaata  aagtatgtag  ctagttaaag  tgcatagtat  atgcttaatc  aatagagtgg      360
tgacagggtg  gagggagggt  ggaggcaggc  tcattcctgc  cctggggccc  agaggagAAC      420
atgtgttaca  gaagtccag  cctacagcca  gctcctagca  ttaaggcagg  tgccattca      480
gctagagcct  canggggggt  cnagttgagg  gagctgctcc  tancctggnc  cccatgccct      540
ttncctttgt  gtggancctt  aagaagcccn  ttttctgan  naanncctgg  gnttananaa      600
ttcacctttg  ncaattacca  agnncccggn  gnaattntcc  ntnttgggng  aaaccnttn      660
nntttaaggg  tgnntnttng  ggattngnac  cnnnnttttg  gggcncncnc  ngntttttn      720
ttttnttnn  aaannccnnn  aaaaanaaaa  aaaaanntnn  gngncnnnaa  annccccnn      780
ggggggggaa  aaaaaaaaaa  antttttccc  cccccccnc  cnc                                     823

```

<210> 125

<211> 691

<212> DNA

<213> Cercopithecus aethiops

<400> 125

```

cctaattccac caacccccaa ctactatagt gggagcctga ggtcacagca tggccccccc      60
gtgttgtgag  aaaaatctcc  acaggattct  cccactgttt  cctaagtgtg  ctctgggac      120
ctcctgact  agtgtggaat  tttgagccag  tgatttctcc  ccacagggtt  caattaaatc      180
atctgtcaaa  tgaggatgac  cacatcttct  ttacctcacc  actgagctgt  gaaatgaacc      240
agaggcctta  ccttttcccc  ctgaactccc  agtcatccct  ggaacaccaa  tttgaacatc      300
atctccact  ttcccagcca  gttagcagct  ctgtcctctg  gatttcaaag  agaaatgtct      360
ctagcatcat  ccctgtttcc  ttgactgtc  ctactttctt  tttcccccca  gagccaggaa      420
tgtcttaaac  agaattgagat  gctccaagg  ggccaccaac  tcacaattag  gagttcaata      480
aatactgact  taagagtga  tgaacgatcc  ccgtgtcttt  gtccacattt  gtacatgctt      540
acatgattct  gcaaagaatc  taaatttctc  ttacattaa  caaacaaggg  ggctgggcat      600
ggtggctcat  gactgtaatc  tcagcatttt  tgtaaccag  gacagtcctg  atgaaataac      660
tgggaaagt  cctttttggg  ggggtggggt  g                                     691

```

<210> 126
 <211> 748
 <212> DNA
 <213> Cercopithecus aethiops

<400> 126
 ccatcgccctt actattgcct tcttgacgag ttcttctgag cgggactctg gggttcgaaa 60
 tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata 120
 gaaaagttca gatcgaggtc aggaacagat ggaacagggt cgaccgggtcg accgggtcgac 180
 cctagagaac catcagatgt ttccaggggtg cccaaggac ctgaaatgac cctgtgcctt 240
 atttgaacta accaatcagt tcgcttctcg cttctgttctg cgcgcttctg ctccccgagc 300
 tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc 360
 ccgggtaccc gtgtatccaa taaacctctt tgcagttgca tccgacttgt ggtctcgctg 420
 ttccttggga gggctctctc tgagtgattg actaccggtc agcgggggtc tttcagcagg 480
 gccgggggccc acagaaggaa aacatctctg tggaatgtgg aaatgcagaa ctctactggg 540
 cccgtttaga aagcacagaa aagcatggaa gaaagggaga ggcgagaagc ctagaaaatt 600
 accctagatc ttaggtatgg atatatcgac ctaaaagaaa gaagatgggg caaagttaat 660
 gcaagcagag agtttatttg gggtaagct tgaggattgc accccaggag catagattca 720
 agttgccctg aatttacact gattagca 748

<210> 127
 <211> 708
 <212> DNA
 <213> Cercopithecus aethiops

<400> 127
 gccaaaccta caggggggggt tctttcactg ccagtcagcg aaccgcgaag ccggcaggca 60
 cttcggcgggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc 120
 ccaggaccca gtcgttttag ctcagggaaa ggaagcggc gacgccagcc tgcaagcttc 180
 actgcgcagc cgtggacacc gccccacgtc gtagggccgt ggaccctgac aacgccggaa 240
 cccggcgctcc ggtgcgtgct cttggcggac cagaatggct aacgtaccgc catgccgcga 300
 ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg 360
 gcactttcct gtccgcgact ccgccccgc cagaggggct aggtccggg tttcaagatg 420
 gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgacct 480
 tacatcacca gcatcgaga cctcacgggc cagggtgtctc tgtacacctt ctgccccaa 540
 gccaaaccagt ggggtgagtgc cgcctggctc tgaggacggc cgcccggccg ctgcggtctc 600

ttaaaggggc cgtgcgtggt gctgtggggg gggggacaca gcaagagcca gggaggtgaa 660
gacggggcca gggactgccg agaagccgac cagaaccaga ggggttgt 708

<210> 128
<211> 741
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(741)
<223> n is a, g, c or t

<400> 128
taacaatttt cacacagaaa ttcaatccaa caaacaanta catattattt tctaagttgt 60
aaagcctgta accgaatgag ttaattagga aggggtcaatt acaagaaagt gggaaattat 120
gctagttggt tttaaacaac taacaaagct tcaagcaggg gctaacgaga atcagtgaac 180
agactgaatg taacttttcg gaccctctcc agtgcacgaa aagccagaaa gtactgagtc 240
tgaggggaac attcagagat gacatcacca gcatcatagg tggaacaaaa cacatttaca 300
gggtctctct tgtttgtaca aaggctcttcg gggatctagt gaacatggaa gcccttttcc 360
taagtgcctt gaaatctttt ccgaaactgt gtagttcgat taaagccgga cccaccgcac 420
tcccccttcc aagaatcgaa actaattgga ttttaagctt taaatccaaa tgacctctga 480
gaaaggggct ctcatctacg tctgccgggg gagaggagga gtgtttattt tatagacaat 540
gtatatgcaa tttatctaataatccgcaaa gcctcaaaca caagctttca ggactcttt 600
tgacccacc ggtctcataa ctoccaatgt atctgcaaag aaggcaggtc gccacgtcc 660
ccaaaccoga cgcaaggga ctgatcctgc tccaatctc cctcactggc ttttccttgg 720
ggatgtgtnc agccacttc t 741

<210> 129
<211> 694
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(694)
<223> n is a, g, c or t

<400> 129
ccgccaacct acaggggtggg gttctttcac tgccagtaca gcgaaccgag aagccggcag 60
gcacttcggc ggtctccagc ctttgccctga aaagagctcg gcaagctagc tagaggtagc 120
acccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgaagc 180

```

ttcactgcgc agccgtggac accgccccac gtcgtagggc cgtggaccct gacaacgccg      240
gaacccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cgccatgccg      300
cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgccctcg      360
atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggctcc gggtttcaag      420
atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cgccctgaa gcaacacgac      480
ccttacatca ccagcatcgc agacctcacg ggccaggttg ctctgtacac cttctgcccc      540
aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggccgctccg gccgctgcgg      600
tctcttaaag gggccgtgcg tgttgctgtg ggggtggggg cacagcaaga ggccagggga      660
ggtgaagacg gggccaaggg actgncgaaa agcc                                     694

```

<210> 130
 <211> 678
 <212> DNA
 <213> Cercopithecus aethiops

```

<400> 130
ccctttactg ccagacagcg aaccgcgaag ccggcaggca cttcggcggc ctccagcctt      60
tgcctgaaaa gagctcggca agctagctag aggtcagacc ccaggacca gtcgttttag      120
ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc actgcgcagc cgtggacacc      180
gccccacgtc gtagggccgt ggaccctgac aacgccgga cccggcgctc ggtgcgtgcg      240
cttgccggac cagaatggct aacgtaccgc catgccgca gggccacgta gaggcggaag      300
ttgatgggac ggacgcagat gggggaacct tgcctcgatg gcactttcct gtccgcgact      360
ccgccccgcg cagaggggct aggtccggg tttcaagatg gaggcgctga gtcgagctgg      420
gcaggagatg agcctggcgg ccctgaagca acacgaccct tacatcacca gcatcgaga      480
cctcacgggc caggttgctc tgtacacctt ctgccccaa gccaaccagt gggtagagtgc      540
cgcttggttc tgaggacggc cgcccgcccg ctgcggtctc ttaaaggggc cgtgcgtgtt      600
gctgtggggt gggggacaca gcaagaggcc agggaagttg aagacggggc caagggaact      660
ggccgaaaag ccaagcca                                     678

```

<210> 131
 <211> 712
 <212> DNA
 <213> Cercopithecus aethiops

```

<400> 131
cccgccagcc tacaggtggg gtctttcact gccagtacag cgaaccgcga agccggcagg      60
cacttcggac ggtctccagc ctttgctga aaagagctcg gcaagctagc tagaggtcag      120

```

```

accccaggac ccagtcgttt tagctcaggg aaaggaagcg cgggacgcca gcctgcaagc 180
ttcactgcgc agccgtggac accgccccac gtcgtcgggc cgtggaccct gacaacgccg 240
gaacccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cgccatgccg 300
cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgcctcg 360
atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggctcc gggtttcaag 420
ttggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac 480
ccttacatca ccagcatcgc agacctcacg ggccaggttg ctctgtacac cttctgcccc 540
aaggccaacc cagtgggtga gtgccgcctg gctctgagga cagccgcccg gccgctgcgg 600
tctcttaaag gggcccgctc gtgttgctgt gggggtgggg gaacacagca agaggccagg 660
ggaggtgaag accggggcca gggacctggc gaaaagcccg aaccagaagc cc 712

```

<210> 132

<211> 738

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(738)

<223> n is a, g, c or t

<400> 132

```

gccagcctac aggggggggt ctntcactgc acagtacagc gaaccgcgaa gccggcaggc 60
acttcggcgg tctccagcct ttgcctgaaa agagctcggc aagctagcta gaggtcagac 120
cccaggaccc agtcgtttta gctcagggaa aggaagcgcc ggacgccagc ctgcaagctt 180
cactgcgcag ccgtggacac cgccccacgt cgtaggggcg tggaccctga caacgccgga 240
acccggcgtc cggtcgctgc gcttggcgga ccagaatggc taacgtaccg ccatgccgcg 300
aggeccacgt agaggcgga gttgatggga cggacgcaga tgggggaacc ttgcctcgat 360
ggcactttcc tgtccgcgac tccgcccccg ccagaggggc taggctccgg gtttcaagat 420
ggaggcgctg agtcgagctg ggcaggagat gagcctggcg gccctgaagc aacacgaccc 480
ttacatcacc agcatcgcag acctcacggg ccaggttgct ctgtacacct tctgccccaa 540
ggccaaccag tgggtgagtg ccgcctggct ctgaggacgg ccgcccggcc gctgcggtct 600
cttaaagggg ccgtgcgtgt ttgctgtggg gtgggggaca cagcaagagg ccagggaggt 660
gaagacnggg gccaggnac tggcgaagag ccgagccaaa gccagagggg tgcgggtcc 720
acctgggaat tgggggaa 738

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<210> 133

<211> 757

<212> DNA

<213> Cercopithecus aethiops

<400> 133

```

cgccaaacct acaggggggg tctttcactg ccagacagcg aaccgcgaag ccggcaggca      60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc      120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc      180
actgcgcagc cgtggacacc gcccacgctc gtagggccgt ggaccctgac aacgccggaa      240
cccggcgctc ggtgctgctg cttggcggac cagaatggct aacgtaccgc catgccgcga      300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg      360
gcactttcct gtccgcgact ccgccccgcg cagaggggct aggctccggg tttcaagatg      420
gagggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct      480
tacatcacca gcatcgaga cctcacgggc caggttgctc tgtacacctt ctgccccaaag      540
gccaaccagt gggtgagtgc cgcctggctc tgaggacggc cgcccggccg ctgcggtctc      600
ttaaaggggc cgtgctgtgt gctgtggggt gggggacaca gcaagaggcc aggggaggtg      660
aagacggggg ccaggggact ggcgaagagc ccgagccaga gccagagggg tgtcgggtcc      720
acctgggatt ggggggatag gaagtgagaa gaagtgg      757

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<210> 134

<211> 668

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(668)

<223> n is a, g, c or t

<400> 134

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ccagcctaca gggggggggt ctttcactgc cagtacagcg aaccgcgaag ccggcaggca      60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc      120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc      180
actgcgcagc cgtggacacc gcccacgta gtagggccgt ggaccctgac aacgccggaa      240
cccggcgctc ggtgctgctg cttggcggac cagaatggct aacgtaccgc catgccgtga      300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg      360
gcactttcct gtccgcgact ccgccccgcg cagaggggct aggctccggg tttcaagatg      420
gagggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct      480
tacatcacca gcatcgaga cctcacgggc caggttgctc tgtacacctt ctgccccaaag      540

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gccaaaccagt gggtagtgatgc cgcctggctc tgaggacggc ccgcccggcc gctgncggtc 600
ntcttaaaag gggcccganc gtgtttgctg tgggggtggg gggacncaag caagaaggcn 660
cagggagg 668

<210> 135
<211> 752
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(752)
<223> n is a, g, c or t

<400> 135
gcttgccaaa cctacagggg gggctcttca ctgccagaca gcgaaccgag aagccggcag 60
gcacttcggc ggtctccagc ctttgccctga aaagagctcg gcaagctagc tagaggtcag 120
accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc 180
ttcactgcgc agccgtggac accgccccac gtcgtagggc cgtggaccct gacaacgccg 240
gaaccgggag tccgggtgcgt gcgcttggcg gaccagaatg gctaactgac cgccatgccg 300
cgaggccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa cttgacctcg 360
atggcaacttt cctgtccgag actccgcccc cgccagaggg gctaggetcc gggtttcaag 420
atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac 480
ccttacatca ccagcatcgc agacctcacg ggccagggtg ctctgtacac cttctgcccc 540
aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggccgcccgg ccgctgcggg 600
ctcttaaagg ggccgtgcgt gttgctgtgg ggtgggggac acagccagga ggccaaggga 660
ggtgaagacn ggggccaggg actggcgaag agccgagcca ganccagagg ggtgtcgggt 720
tcacctggga ttgggggata ggagtgagag aa 752

<210> 136
<211> 739
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(739)
<223> n is a, g, c or t

<400> 136
ctttcactgc cagnacagcg aaccgcgaag ccggcaggca cttcggcggg ctccagcctt 60
tgcctgaaaa gagctcggca agctagctag aggtcagacc ccaggaccca gtcgttttag 120

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ctcagggaaa ggaagegecg gacgccagcc tgcaagcttc actgcgagc cgtggacacc 180
gccccacgtc gtagggccgt ggaccctgac aacgccgga cccggcgctcc ggtgctgctg 240
cttggcggac cagaatggct aacgtaccgc catgccgga ggcccacgta gaggcggaag 300
ttgatgggac ggacgcagat gggggaacct tgcctcgatg gcactttcct gtccgcgact 360
ccgccccgc cagaggggct aggctccggg tttcaagatg gaggcgctga gtcgagctgg 420
gcaggagatg agcctggcgg ccctgaagca acacgaccct tacatcacca gcatcgaga 480
cctcacgggc caggttgctc tgtacacctt ctgccccaa gccaaaccagt gggtagtgct 540
cgcctggctc tgaggacggc cgcccgccg ctgcggtctc ttaaagggc cgtgctgtt 600
gctgtggggt gggggacaca gcaagaggcc agggaggtga agacggggcc agggactggc 660
gaagagccga gccagagcca gaggggtgtc gggccacct gggattggg gataggggtg 720
agagaagngg ctgganaat 739

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<210> 137
<211> 707
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(707)
<223> n is a, g, c or t

```

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<400> 137
gccccaccta caggtgggat ctttactgac cagacagcga accgcgaagc cggcaggcac 60
ttcggcggtc tccagccttt gcctgaaaag agctcggcaa gctagnntag aggtcagacc 120
ccaggaccca gtcgttttag ctgaggaaa ggaagcgccg gacgccagcc tgcaagcttc 180
actgcgagc cgtggacacc gccccacgtc gtagggccgt ggaccctgac aacgccgga 240
cccggcgctc ggtgctgctg cttggcggac cagaatggct aacgtaccgc catgccgga 300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg 360
gcactttcct gtccgcgact ccgccccgc cagaggggct aggctccggg tttcaagatg 420
gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct 480
tacatcacca gcatcgaga cctcacgggc caggttgctc tgtacacctt ctgccccaa 540
gccaaaccagt gggtagtgct cgcctggctc tgaggacggc cgcccgccg ctgcggtctc 600
ttaaagggc cgtgctgtt gctgtggggt gggggacaca gcaagaggcc agggaggtga 660
agacggggcc agggactggc gaagagccga gccagagcca gaggggt 707

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<210> 138
 <211> 818
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(818)
 <223> n is a, g, c or t

<400> 138
 tcacacagaa ttcagnaaag cacagctgtc taggcgtttg gtcctgaca aatgggtgcc 60
 tgccccctcac ctcaccagcc tctccagaca cctctgcac acacagcact gatgaccgcc 120
 tcccagccca acaccactc tgcttactct gtgcgccag gctctgattg tgtttgggag 180
 gtaaagtgtc cagccccaag actggccaaa ctggccctc atcatcccat tcctccttgc 240
 cagtgggttta tctaggaata gatatggggc cctgttcagg tcagtgaat gtaaggtga 300
 gttagtccag gaatttctga gaaagattct cctctgtaat aaagcagaga gtcacatgac 360
 tagaaaatct ttttgttgtt gttgttgttt taccaccacc ccttccttcc tgctttggaa 420
 atcggtttat gatgtgatgc ctggagctgt ggcagctgtt ttatgaccat gagagaaggc 480
 tttccagtg tgctaggatt caggggagga aatacagaat gaatgtcagc cctcgatgac 540
 actgccgagc cctaaaccaa ctctgagaat ttaagacttt ttgttctgta agaaatgaga 600
 tttatttatt gtttaagact ctgttgggta ttctgttacc tgtggccan aatattttaa 660
 ataataataat ttctttttgc aataatacat ctcagatgga cattcccca agtctaagac 720
 tttgagagaa gtcattctctg aagagccaag cattcataat tagaaacttg gccaggtgca 780
 gtggctcacg cctgtgatcc cagcactttg ggaggcca 818

<210> 139
 <211> 581
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(581)
 <223> n is a, g, c or t

<400> 139
 cacacaaatt agnncaggtc atcctcctgg tggttcctgt accagtcctc gatcacctcc 60
 tcaaactctt ccaccagcac gtgcgactgt taatcgtaac acctcacgtt ggcaaagccc 120
 cagcacctta ctactccta gaggagctca gctaagcctt gcaacccact gcaaggtagt 180
 .ggcagtggtt cacctaagga aactgaggct agagaggtga aatgacgtga ccaaagccac 240

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cctggcctgg gtggccctcc tcagagcaga cccaatcccc accggcccct cactgggcac 300
agcaaccctt ccaagggctg aagggcctgt acctgcttct tgaggtcagc cacctctgca 360
gaagtctcgt tccacagctc ataggggatg tccatcacca ccttgacccc tttgtgtacc 420
aggttgtgta atgtctcaaa ggtctctgac atgccctgga agaagcgacc agacatggga 480
ggcagagctc ccttctctcc ctctaccct cctctcccag tggggcctat gaactcagct 540
gtaagaccaa tgcccaatgc cctctgagga tcctcaaacc t 581
```

<210> 140
<211> 630
<212> DNA
<213> Cercopithecus aethiops

```
<400> 140
tcacacagaa ttccatgttc agtaaccagg tgctacaaat gcagttcaag gctctaggtc 60
atgacaatgt cacagatatt tcaggtccag tcaccaaggc aacatgtggc ttgggtcttt 120
ttctggtttc aagactgcat ctgtattctc tcacctccct gggcccacag attccctaaa 180
tcatagcttg gtctaagagc aatgcttcaa attcaggtcc cttgtctcag gtgggtagac 240
ttctgtcac ccagccaccg ccacctgatt ctggacctgg agccggcagg cccgtggctt 300
cagcccgact cactcttttg tattctgttg ctactatca tctttttttt ttttggctct 360
gaactccgca gtgtcatttt tttttcttag tttatccatc tttgccatgt gtttggggaa 420
gaatggcaat gcgaaagtgt gaacttcag tcccggtta ttagaagccc acagctgttt 480
taaaaaaat ctaccttgct atcctttccc ttttctgtga cacacaagtg actgttaatt 540
agtacctagg ccattgggctg tcattgctaa aaactgaatg gaattttttg ttcttttagc 600
aatgttagga tgactggctg attataaaaa 630
```

<210> 141
<211> 737
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(737)
<223> n is a, g, c or t

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<400> 141
acacagaatt ctacttaat acatataaac agaacatttc taggtcagtg aacaaaaata 60
taacctgaat cataaaaaa gagttataac tcctccatca atttcagac atcagccagt 120
ttacaaatcc agaaccctt aaatgaagaa caagcttgat gcccttgagg aagggcccta 180
gtacactgcc caaaatctgt acatttaatt ttcctcctaa tcttcccaa aggacatat 240
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gtcctttttac cagtgaact gctcatttgg gtaattgaaa ataatcaa at cagggtactac 300
 tggaccctgg ctacgaactg atgcaaattc caggagacct aacatgccat ggtgggtccac 360
 aaagacagtg cttatgggaa tcagggtgatc catggagttt taagttgggt ccaactcaca 420
 tttgaataaa tatactcatg ctgacagaat ctccataatg gttccctgac ctgtaaagt 540
 aggtgcatta tgggtgggtaa tggcaaattg aagccagtag aacacctct atctaggaaa 600
 aatagtaaag caaatgcaat attttcatct ccgtagggat tgcagacatt agttgccacc 660
 atcaagggtc tgaaaaatga ccaggggggtg attcccacca acattctnca ttcagctttg 720
 tctattnggg ccttgcc 737

<210> 142
 <211> 768
 <212> DNA
 <213> Cercopithecus aethiops

<400> 142
 tttcacacag aattcagtgg atgctatgaa acatatcttc actgttcgtg tttgtctctt 60
 tctgaatcca caagtgatgg acacatgaat ctactactac tgttctcttt tcttcttttt 120
 ccgtctttct ctcccttccc acccctagtt cctgacgttt gcctactcta tcatgtctgc 180
 agtgttgcat accactctgc atcctcatct gtctgagaca cattcaacca ctaggtcttc 300
 agctgcttca ctgctgcctg atgttctttg aagtcagta taagagagaa cattctattt 360
 tgctaaaact aaaagactac cctttatctt tgctgagaat atgtaaagaa aaggggaatg 420
 actagatcag aaggcttatt ctgaggtata tagtaatgtt aattttttaa taattgttag 480
 gtgttcttct tcattaggtg ttcaccttca gttttccaag actatggaaa gcaccattgg 540
 tgcattgtagt taacagcagc ttgactcaga cgtagaactg cagccaggac ccattctgttc 600
 cccattactc cctgctgcca gttttgcaac cagaacctag gaggatgatt tcccatcttc 660
 aattttgctc aggactcagc agaagaagga tcctgggaca caagactttt cagtggcttc 720
 aaacttggga gagttctttg gcaatgcaca ggtttgacct atgaactg 768

<210> 143
 <211> 450
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(450)
 <223> n is a, g, c or t

<400> 143
gcctgtgaaa ccatctggnc ctggactttt tttggttggn aggctatcaa cttattgcct 60
caatttcaga gcctactatt ggtctattca gggatctcaa ctncctctctg gcttttagtct 120
tggaagagtg taagtgtcca ggaaatctat ccatcttctt ctagattttc cagttttattn 180
cgcgagagg cgttcacagc agcctctgat ggtagttcga atttctgagg ggnccggcggn 240
gatatccctt ttatcattnt naatngcgnc gatnagacnc ttctctcttn tcttctttat 300
aagcactcng ctagccggcc ngccaatntc-gnngangctt ntcaaaaaac caactcctgg 360
attcatcgat tncnntggag ggtctntttg ngctctctatc tcccttcagtn actgcnctga 420
tcttagmata tttcntgccn tctgctagct 450

<210> 144
<211> 729
<212> DNA
<213> Cercopithecus aethiops

<221> misc_feature
<222> (1)..(729)
<223> n is a, g, c or t

<400> 144
cacacagaat tacccttttc gccttccaag gggaaaccag gccactttgc tcttcttggg 60
gaaggaggat aattgtccag tgctgggagg tgacagcagc tactgccagc acgagggtggg 120
gccctgcag tgtggttctt caggtctgag aggggttccc tctgccttcc tccctcctgc 180
tcccctttcc tcttctctct acctgttttt tcttctctc acatctctcc tgcttcccca 240
caatccctga catttactgc aggtcccca agagccatga cactttatac cctcaacctc 300
atttaattct caggaaaccc cacaaggccg tgcaattctc accccaggta ccaagtgcgc 360
cagttcaggt gcacagagac tgccccttgc ccagagatcc tagcacgagg gctctgtact 420
ggtttagggc tccagagaaa cagctccaat agaatgtgca gatgctgggt gcagtggctc 480
accctgtaa tcccagcact ttgggaggcc gaggcgggcg gatcatgagg tcaggagatc 540
gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaatacaa aaacattagc 600
cgggccgtgg tggcgggncg cctgtagtcc cagctacttg ggaggctgag ggcaggagaa 660
tggcatgaag ccganaggca nagcttgagc tgagccaaga tcacatggca ctccaacctg 720
ggcgacaaa 729

<210> 145
<211> 755
<212> DNA
<213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(755)
 <223> n is a, g, c or t

<400> 145
 aacaattttc acacagaatt acctgggtctc aaagtgtatc ctccatgctt cggcctccca 60
 aagtattgtg attacaggag tgaccacccc tgcccggccc tctagcttat ggtggaagct 120
 taaataatca gtttttagaca tttcttcttc ctttttttcc caagaaacag ggtcttgctc 180
 tgccaccac gctggaatga agtgggtgcaa tcatagctga ttgcaacctc aaactcctta 240
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 cgcacctggc ctcttctttc taatataagt atttaatat ataaaatttc ctctaagatc 360
 taaacactgc tttagctgca actcacaat tttgatatgt tgtattttta tttatatccc 420
 attaaaaata cagtattagt tcccggtgta tttcttcttt gacctatggc ttagaagtgt 480
 gttgtttagt ttccaaattt gggggcattt tccagatata tttctcttat ttatttgtaa 540
 tttaattctg ttgtggtcga ggagcacgtt ctgtttgctt acaatcctcg taaatttatt 600
 atgacttggt ttatggccca gcatagggtc tgtttggcga gtgttccatg tgcacttgaa 660
 aagaatgtgt attctgtagt tgtgcagggt atttttaaaa ttttattctt ttcactgana 720
 caaaatagct gtncatattt agagggtaca tgcca 755

<210> 146
 <211> 795
 <212> DNA
 <213> Cercopithecus aethiops

<400> 146
 ctaccagtat atacaaagaa aagctcgtac cattcatgct gaaactactc caaaaagttg 60
 aggagaagga aatcctccct agcttattct acaaagctag catcacactg ctacaaaaac 120
 ctgacagagt cacaacaaca aaaatttcag acatatattc ttgatgaaca ttgatgcaaa 180
 gtagtcaaca aaatacttgc aaaccaaatt cagcagcaca tcaaaaagct tatccatcat 240
 gatcaagtag gctttatccc tgggatgcaa ggttgggtca acatctgcaa atcaataaat 300
 gtgattcatc acataaatac cactaaagac aaaaaaacca catgattatc tcaacagatg 360
 cagaaaaggc ttttgataaa atccaatacc ccttcatggt aaaaactctc aataaactag 420
 gtattgaagg aacatacctc aaagtaataa gaaccaccta taaaaaaccc acagccaaca 480
 tcatattgaa tgggcaaaag ctggaagcaa tccccttgaa aactggagga agacaagaat 540
 accctttctt accactccta ttcaacataa tattggaagt cctggccagg acaagcaggc 600

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aagagaaaga aagaaaggca tcccaatagg aagaaaggga agtcaaacta tccctgtttg 660
cagacaaaat gatcctatag ctagaaaccc catagtctca gcccaaagct ttttaagctga 720
taaacacttt cagcaagcct cagcatacaa aatcatgtgc aaaagtcagt acattttgta 780
caccaccaac agtca 795

<210> 147
<211> 704
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(704)
<223> n is a, g, c or t

<400> 147
gcacccctccc tccctggcct gggcggtggc tcgcaaaacg ctgggattcc cggatttaca 60
ggcggggcgcg ccacgccagg agcaaacact tccctgttta aaaattcagt gttgtgattg 120
gctgccattc agcattatgc taattaagca tgcctgtttt ttttaagctt cttaaaacaa 180
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ctgttaagac tatactttca gggatcattt ctatagtttg ttactagaga agttctctct 420
gaacgtgtag agcaccgaaa accacgagga agagacgtag cgttttctcc tgagcgtgaa 480
gcgggcggtt ggtgttgctt cgctgcaact gccatcagcc attgatgatc gttcttctct 540
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tagaacgaca gactgtacag cgaccgtntc ccggcttgnc tntgtgcttg nntgnccnc 660
ngaggccnaa gngagttgcc ttattttgtt tccagnanccg ntgt 704

<210> 148
<211> 650
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(650)
<223> n is a, g, c or t

<400> 148
atgccttct atgccttct tgacgagttc ttctgagcgg gactctgggg ttcgaaatga 60
gctagccctt aagtaacgcc attttgcaag gcatggaaaa atacataact gagaatagaa 120


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aagtteagat cgaggtcagg aacagatgga acagggtcga cgggtcgacc ggtcgaccct 180
agagaaccat cagatgtttc caggggtgccc caaggacctg aaatgaccct gtgccttatt 240
tgaactaacc aatcagttcg cttctcgctt ctgttcgcgc gcttctgctc cccgagctca 300
ataaaagagc ccacaacccc tcaactcggg cgccagtcct ccgattgact gagtcgcccc 360
ggtacccgtg tatccaataa accctcttgc agttgcatcc gacttgtggt ctcgctgttc 420
cttgggaggg tctcctctga gtgattgact acccgtcagc gggggtcttt cagttaagac 480
tatactttca gggatcattt ctatagtttg ttactagaga agtttctctg aacgtgtaga 540
gcaccgaaaa ccacgaggaa gagacgtagc gttttctcct gagcgtgaag cgggcgtttg 600
gtgttgcttc gctgcactgc catcanccat tgatgatcgt tttntntccg 650

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<210> 149
<211> 671
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(671)
<223> n is a, g, c or t

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<400> 149
aactttaact aatggcgaga taccttcgct attgccgatg ccattaggaa acaaatagaa 60
aaatagtctg gcaacaacat cttctcgaat attatcactc gacaaattat aacgttttag 120
gtggaaacgg aactttaaaa aattgtttta agaagcggaa aaaaaacagg catgcataat 180
tagcataatg ctgaatggca gccaatcaca aactgaatct ccaaagcagg aagtgtttgc 240
tcctggcgtg gcgcgcccgc ctgtaatccg ggaatcccag cgttttagcga gccacgccc 300
aggccgagga gggaggatcc tttgttccac gagatcgaca ccagcctagg caatatagca 360
gaatcctggt ggtgacggaa atgccctatc ttgagcttat caatgccaaa accccggtca 420
tataacttta ttggatatca gtggggaaaa ctgagtaaaa ggtgcaaatg tataactcag 480
tataaacccc aagaacgaaa cgcaaacct accattctct gaaagaaatg tttgtacat 540
atatttacac agaaacacat acatcatgat caaaaaatga catcattcgt aaaaaaaaaat 600
aacaaaaagt gtaaaagaac ccacgcgccg gaaaggaagg gccctgtgag accggatccc 660
caaaacaaaa c 671

```

```

<210> 150
<211> 704
<212> DNA
<213> Cercopithecus aethiops

```

<220>

<221> misc_feature

<222> (1)..(704)

<223> n is a, g, c or t

<400> 150

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tcattaacag cccactcgca gcctctgcgg ggtctacatc tgctgccaac ttttaactaa   60
tggcgagata ctttcgctat ttccgatgcc attaggaaac aaatagaaaa atagtttggc   120
aacaacatct tctcgaatat tatcacttga caaatTTTaa cgttttaggt ggaaacggaa   180
ttttaaaaaa ttgttttaag aagcttaaaa aaaacaggca tgcttaatta gcataatgct   240
gaatggcagc caatcacaaa ctgaattttt aaagcaggaa gtgtttgctc ctggcgtggc   300
gcgcccgcct gtaatccggg aatcccagcg ttttgcgagc ccacgccag gccgaggagg   360
gaggatcctt tgttccacga gttcgacacc agcctaggca atatagcaga attctgtgtg   420
aaattgttat ccgctcacia ttccacacia catgagcgtc agaccccgaa gaaaagatca   480
aaggatcttc ttgagatcct ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac   540
caccgctacc agcggtggtt tgtttgccgg atcaagagct accaactctt tttccgaagg   600
taactggctt cagcagagcg cagataccaa atactgtcct tctagtgtag ccgtagttag   660
gccnccact tcaagaactc tgtagcaccg cctacatacc tcga   704

```

<210> 151

<211> 705

<212> DNA

<213> Cercopithecus aethiops

<400> 151

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gctatattgc ctaggctggt gtgaactcg tggtaacaaa ggatcctccc tcctcggcct   60
gggcgtgggc tcgcaaaacg ctgggattcc cggattacag gcgggcgcgc cagccagga   120
gcaaacactt cctgctttta aaattcagtt tgtgattggc tgccattcag cattatgcta   180
attaagcatg cctgtttttt ttaagcttct taaaacaatt ttttaaaatt ccgtttccac   240
ctaaaacggt aaaatttgtc aagtgataat attcgagaag atgttggtgc caaactattt   300
ttctatttgt ttctaattgg catcggaat agcgaaagta tctcgccatt agttaaaggt   360
tggcagcaga tgtagacccc gcagaggctg cgagtgggct gttaatgaaa gacccacct   420
gtaggtttgg caagctagct gaggatcgtt tcgcatgatt gaacaagatg gattgcacgc   480
tggttctccg gccgcttggg tggagaggct attcggctat gactgggcac aacagacaat   540
cggctgtctt gatgccgccg tggtccggct gtcagcgagc gggcgcccg tttttttgt   600
caagaccgac ctgtccggtg ccctgaatga actgcaggac gaggcagcgc ggctatcgtg   660

```

gctggccacg acgggcgttc cttgcgcacc tgtgctcgac gttgt

705

<210> 152
<211> 673
<212> DNA
<213> Cercopithecus aethiops

<400> 152
tttcattaac agcccaactcg cagcctctgc ggggtctaca tctgctgcca acttttaact 60
aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatacaa aaatagtttg 120
gcaacaacat cttctcgaat attatcactt gacaaatatt aacgttttag gtggaaacgg 180
aattttaaaa aattgtttta agaagcttaa aaaaaacagg catgcttaat tagcataatg 240
ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcgtg 300
gcgcgccccg ctgtaatccg ggaatcccag cgttttgca gccacgccc aggccgagga 360
gggaggatcc tttgttcac gagttcgaca ccagcctagg caatatagca gaattcatct 420
cacagagtta catctttccc ttcaagaagc ctttcgctaa ggctgttctt gtggaattgg 480
caaagggata tttggaagcc catagagggc tatggtgaaa aaggaaatat cttccgttca 540
aaactggaaa gaagctttct gagaaactgc tctgtgttcc tctgaattct ggaagaaaac 600
aaacacatca ttctgtctc caagagctta aatttctgtt tgggcaattt atttataaaa 660
acacaactta gcc 673

<210> 153
<211> 709
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(709)
<223> n is a, g, c or t

<400> 153
tttcattaac agcccaactcg cagcctctgc ggggtctaca tctgctgcca acttttaact 60
aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatacaa aaatagtttg 120
gcaacaacat cttctcgaat attatcactt gacaaatatt aacgttttag gtggaaacgg 180
aatnttaaaa aaagttttta agaagcttaa aaaaaacagg catgcttaat tagcataatg 240
ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcgtg 300
gcgcgccccg ctgtaatccg ggaatcccag cgttttgca gccacgccc aggccgagga 360
gggaggatcc tttgttcac gagttcgaca ccagcctagg caatatagca gaattctgtg 420
tgaaattgtt atccgctcac aattccacac aacatgagcg tcagaccccg aagaaaagat 480

caaaggatct tcttgagatc cttttttttc tgcgcgtaat ctgctgcttg caaaacaaaa 540
aaaccaccgc taccagcggg ggtttgtttg cncgggatca agagtctacc aacctctttt 600
ttacgaaagg tnaactgggct tcaggcagga gccgcanatt nccaaaataa ttggnccctt 660
ccaagngggn ancccgcnag gnttagggcc cncccaactt tcnaaggac 709

<210> 154
<211> 574
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(574)
<223> n is a, g, c or t

<400> 154
cctcggcctg ggcgtgggct cgcaaacgc tgggattccc ggattacagg cgggcgcgcc 60
acgccaggag caaacacttc ctgcttttaa aattcagttt gtgattggct gccattcagc 120
attatgctaa tnaagcatgc ctgttttttt taagcttctt aaaacaattt tttaaaattc 180
cgttaccacc taaaacgtta aaatttgtca agtgataata ttcgagaaga tgttggtgcc 240
aaactatttt tctatttgnr tcctaattggc atcggaaata gcgaaagtat ctcgccatta 300
gttaaaagtt ggcagcagat gtagaccccg cagaggctgc gagtgggctg ttaatgaaag 360
acccacctg taggtttggc aagcatagct gaggatcgtt tcgcatgnrr gaacaagatg 420
gattgcacgc tggntctccg gccgctngng tggagaggct attcggnrat gactgggcac 480
aacagacaaa tcgggctgnr ctgatgccgc cgtgttccgg ntgtaagcgc aggggcgcgc 540
cngtttcttt tttgnaaaga ccganctgta acgg 574

<210> 155
<211> 794
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(794)
<223> n is a, g, c or t

<400> 155
actccggaga tatgaggcct agctccatcc ttcttttctt atcactcagt cattcaatct 60
ttgcttgga aacatgaact aataatttcc aatattacct gacatggatc cactttaggg 120
aagacacaag atatgaaaga aaggataaag tctgaaagtt agaagtaaca caactacaga 180

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| | |
|--|-----|
| aatagatta atgtggattg ttatagccat tcatacaatg acatccctcaa cgtcaaaacc | 240 |
| tttttggact ctttacagat tccacatcca agcagaatc tatttaaatgt gctttctaac | 300 |
| aatcagattc ctgacaaatg tggtcataaa gtaataaaag cagcaaaatc ttaaattgtt | 360 |
| tatactaaca tagtagacaa aatacaaaata ctctgaacac taatatcaca gaaaccctta | 420 |
| aaaaaaagat tgaggggagg taataacata cctaatacaa atagaaataa ggaggaacct | 480 |
| ttgaggtttg ctatgctttg aacgtgtccc caaggttcac atgttggaac cttaatccct | 540 |
| gaagcaacag tgatgagaag tgggaccttt aagaggtgag taggtcacga gggctctgct | 600 |
| ctgccacatg aatggattaa tgctattacc agaggagtgg ggaatgggtt ccagatagaa | 660 |
| gaccgagttt ggcctcctcc ttatntntcg ctctctngcc ttccgccttc taccatggga | 720 |
| tgatacagca ggaagacctt agataccaca ccttgatatg gacttcngt ccnanaacct | 780 |
| tgantaaata ccag | 794 |

<210> 156
 <211> 831
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(831)
 <223> n is a, g, c or t

| | |
|---|-----|
| <400> 156 | |
| cgcacgcct tctatgcct tcttgacgag ttcttctgag cgggactctg gggttcgaaa | 60 |
| tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata | 120 |
| gaaaagtcca gatcgaggtc aggaacagat ggaacagggt cgaccggctg accggctgac | 180 |
| cctagagaac catcatatgt ttccagggtg cccaaggac ctgaaatgac cctgtgcctt | 240 |
| atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg ctccccgagc | 300 |
| tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc | 360 |
| cggggtaccc gtgtatccaa taaacctct tgcagttgca tccgacttgt ggtctcgctg | 420 |
| ttccttggga gggctcctc tgagtgattg actaccgctc agcgggggtc tttcaaggtc | 480 |
| aactgacttt aaacttgccg tttgatttgt gacttttagaa agtagagtta actatatatta | 540 |
| gcaatatgct taagcatgtg catatcacct catgaaacgt gtgtgtgcat gagaaaagct | 600 |
| gcctccagta catatacata tgtatataaa cacacataca cacaagcata tatatgtatg | 660 |
| tatttcttgn aggaccagtc tcattgtata taatttcaag tgcaggttcc tgatctccan | 720 |
| ggatgcgtaa aagactcact gaagttnnga agaaanttta nggctactat tntgttgng | 780 |
| atcncacctt tcaagtttaa atttgatntg attattctta cngnttgcn g | 831 |

<210> 157
 <211> 637
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(637)
 <223> n is a, g, c or t

<400> 157
 caacctaaga aaaactcaca gccactttta aagcagtaac acatgtataa agtatagttt 60
 ggatcctttt gtacacagct cctgaaagag agaaattttt ttttcaccta ccgacagaca 120
 tattggaagg ctgctaatat tctgactttt acggactgta ctccctttaa cctgggtaca 180
 taccataata ttcttttcagt tgnccacagc tatagatacc cctagcataa cacttcagga 240
 ttcagaagac gaatgtacct ttctgtatct taacctctct actccacact tcccacctct 300
 gaaaaaacia caggccaaat tctcagaacc taaaaccaag tcagagtaaa cactgctaata 360
 acaataactga cacttacata tttacctggc ataattcteta ggattccacc cacaacctaa 420
 cagatcctaa ctctctcata gagngagaaa atctgctaaa atctgacaga agtccaaatg 480
 aatcctttca gatatatgta gcttgctaca cactcagaaa gnnaagttct cggaacttga 540
 aagctctctg aaactnttac cagntacaag angttncagc nnatcacact agcagcatgg 600
 ntaanggcaa accagagcag ctaccggaan attaaag 637

<210> 158
 <211> 656
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(656)
 <223> n is a, g, c or t

<400> 158
 tccatacctt taaaattcaa gaatgttgtg ttctaattggc agtttgaccg ttgagatatt 60
 aacataggaa catcatttag cctcttaagc ttgaacatcc attaaagcggg aaaaatagtg 120
 cttatttctc agaggtttgc agacattggc taaccaatag ttntgatntt gctggaaagc 180
 aatgtgcaaa ttttcttaga tgtgatcgct tcattttctc ttacatttta gattggcagc 240
 agccaaatgg gcgttccagc ccctnatctc ctgcaagatt cttctcagtt tcataaatct 300
 ggtaattttt gagctctttt cccaacaggg tgctgcagct caccaagtgg aatctacaac 360

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atcttctgct accaggatag cagcttgcca gcaggatata ctgaaattac tgggtttcag 420
tatgatgttg gctggtacga acntcaatca tncgaatcga catgcgcccc gccattctca 480
taatgaaatg tntcctttctc ctttcaacat gttccgcttt ccagcccccc atcctccntt 540
tattatnttt tttctttcan nnaaaagaag ctttnagnaa acacnnaaac ctcttactcc 600
ctntagnгаа agggaaacnt tctttccnnt nctnctccc ctttngannc ncccta 656

<210> 159
<211> 654
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(654)
<223> n is a, g, c or t

<400> 159
cattttaatt tttatatagg atggtattta tgaacatccc actaactatt ctgccgctga 60
ttgatatttg gatgtgtaca gtttgatgct attataaaat tcttctaaga acattcttgt 120
acatgttcat tttgtttcgc taggtcctag agtctaagggt atatatccag aagaggaata 180
gctgggtatt atgatagaat aatgacaaac tagtttctaa agtgattgta ccaattagtg 240
tttccatagg agaaaagtgt acagctactg gaaaaacagt ttggaatgat ctgaagtata 300
agaatgttca tagcaacaga atgtgtttct tgtattccaa atgttcacct acagttgggtg 360
tggtcagtat aagtgttgtt ttttgttttt attgtgtgtg tgtttttttt atcctttggg 420
acagggcctc actttgttat ccaggctaga gagcagtggt acaaacatga ctactgcag 480
ccttagcctc ccaggctcaa gcagtcctcc tgccctagcc tcctaagtac ctgggactac 540
aggcatgtgc caccacacct ggctaatttt tgtattttnt tgtagagaca gggtttcacc 600
atgttngccc agtctggtct agttttaaac aaagttgtng cctgngggaaa tgat 654

<210> 160
<211> 683
<212> DNA
<213> Cercopithecus aethiops

<400> 160
ttactgcata tgcacacaaa aaccacccga agaaaaaag tgtgaatgcc atacaatttt 60
tttcaatgca agtatggaac actgtacatc actgaaaaac aggggggaaaa aaaaaaagga 120
aaaagaggag aaccattgaa gaaagcataa aatagcagct agctttctta cgtgtgctgg 180
aattgtgtct ttcgggttaa ccccaaattt tcctatgcta tacactcttc tcacattttg 240
gtcaatacta gcttctgaat tggaagaggc attatcaatt gctttaaaat gttataceta 300

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aaataaagaa acactgagtt agactgtcac cactttgaat acccatcagg agagtgtggc 360
attgcatgcg aaaatgtatg tggttcctctt aggagatgaa gatcaagtca gctaacagct 420
gtcaacaaac ttctagtgtg ggcaagaatt ttatggccaa gtggggcttt cctttattcc 480
ttactggaag aaagtattca gaaaatagca ttttagggga aaaaagtgtt aagtaaacag 540
aatcctttta agcacacaaa caaagtgtga gcagtgtaaa ttttgaaact tagtgccttt 600
tagtatctga agcaaaatga taacaagtta taggattttt tctttatgaa gaatgatgta 660
agctcactta tgaaagaaga acc 683

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<210> 161
<211> 811
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(811)
<223> n is a, g, c or t

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<400> 161
ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60
atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120
tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg 180
gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctaccag 240
tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggttc tctatcttcc 300
ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360
aattcatact gcaaaacaac ttagttnta ccatgtgccg ggcatgtgcc ctagttgtctg 420
acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480
attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
agaaaaaaaa gaggaagggt ctgatttttg tgtctttccc tccanaatgc aagctccctt 600
gaggatacag atttgngtgt tttttaacta ctgnaatnct ccctgacaat agcgccccag 660
tnacatagta agggcatttc gannccaatt ttttaaaaat gaagaaaact aggccagtta 720
ccncagtttc ctggggccca attttcaact ttttagganc ntnaantacc gatataaana 780
aaattcgggt acagctaggg ctccgnatna a 811

```

```

<210> 162
<211> 757
<212> DNA
<213> Cercopithecus aethiops

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<220>
 <221> misc_feature
 <222> (1)..(757)
 <223> n is a, g, c or t

<400> 162
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60
 atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120
 tgctcctcat tctagcctct ggatctttgc ccttgctggtt ccttacgctc ttctcccagg 180
 gatctgaaag gctcacaccc tcacctcctt cagagggttg ctaaaatgtc ttctaccag 240
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggttc tctatcttcc 300
 ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360
 aattcatact gcaaaacaac ttagttttta ccatgtgccca ggcattgtcc ctagttgctg 420
 acaatacagt tgaaaataaa atagacaaaa atcccatcctt ttgaatcttt tgaaccttac 480
 attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
 agaaaaaaaa gaggaagggt ctgatttttg tgtcttccct ccagaatgca agctccttga 600
 taggcattcg atccaatttt aaaatgagat actaggcagt tactcagttt tctgggcaca 720
 tttcaacttt tagacaataa taccgataag aaaanta 757

<210> 163
 <211> 749
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <222> (1)..(749)
 <223> n is a, g, c or t

<400> 163
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60
 atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120
 tgctcctcat tctagcctct ggatctttgc ccttgctggtt ccttacgctc ttctcccagg 180
 gatctgaaag gctcacaccc tcacctcctt cagagggttg ctaaaatgtc ttctaccag 240
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggttc tctatcttcc 300
 ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360
 aattcatact gcaaaacaac ttagttttta ccatgtgccca ggcattgtcc ctagttgctg 420
 acaatacagt tgaaaataaa atagacaaaa atcccatcctt ttgaatcttt tgaaccttac 480

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attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
agaaaaaaaa gaggaagggt ctgatttttg tgtcttcctt ccagaatgca agctccttga 600
ggatacagat ttgggtgttt tntactactg natctcctga acaatagcgc cccagtagct 660
aggtaggnca ttcgatccaa nttttnaaaa agaggancct agggccagtt aactnaagtt 720
ttctggggcc ccatttccaa acttttaga 749

<210> 164
<211> 741
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(741)
<223> n is a, g, c or t

<400> 164
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tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt 120
gctcctcatt ctacgctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg 180
atctgaaagg ctacacacct cacctccttc agaggtttgc taaaatgtct tctaccagtt 240
gaagccttcc ccaaccacca cattaaaaac acacaaccag caccggttct ctatcttctt 300
tcacttttga tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta 360
attcactactg caaaacaact tagtttttac catgtgccag-gcattgtccc tagttgctga 420
caatacagtt gaaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca 480
ttgggagtgga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa 540
gaaaaaaaaa gaggaagggt ctgatttttg tgtcttcctt nccagaatgc aagctccttg 600
aggatacaga attngtgtgt ttttttacta ctgnatctcc tgacaatagc ncccagtaca 660
tagtaggcat tcgatccaat ttttnaaaaga ganactaggc angtaactaag tttntggggc 720
cattnnactt ttaagacaat a 741

<210> 165
<211> 727
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(727)
<223> n is a, g, c or t

<400> 165
ctacgataca tgtaacattc tacgaacaac catggtgagt agaaccatct ggattttcca 60
tcactttcat ttaaaagact ctgttgatat tctaggtagt gattccatat atcagtatca 120
acaaatttct caaccaaggg gataattggg ttatctgttt gcaattcatt ccgtaattta 180
gaaaggagag aaatagcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa 240
atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcg tgtctatgca attcctctag 300
ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc 360
tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata 420
tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt 480
actacagagg gaaaggaacc cctgacagat tttccatgtc tttcatgctt ccatacacat 540
tcttctttca ccattgacac cactagaaaa gaaactgtgg cctttctgag gtttcttttg 600
gtagctcaat tttttttttt aacttgtttt ccactgagtt ctagctaggt gagagatgag 660
atatgctgac atacaaggcg ctacaatata tctcacatga caggccantg ggagtgggga 720
naaatgt 727

<210> 166
<211> 713
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(713)
<223> n is a, g, c or t

<400> 166
cacgagaatt ctgtctcaaa aaaaaaaaaa aagccaaagg tcctctaaaa tggcctgcat 60
ggcactacat tctctggccc tttatcagca ctctgacagc tctctccttt gcttattttg 120
ctcctcatte tagcctctgg atctttgccc ttgctgttcc ttacgctctt ctcccagggg 180
tctgaaaggc tcacaccctc acctccttca gaggtttgct aaaatgtctt ctaccagtg 240
aagccttccc caaccaccac attaaaaaca cacaaccagc acccgctctc tatcttcctt 300
cactttgcat ttgtccattg tgtaacatca cttacatacc tttaattttt agtttattaa 360
ttcatactgc aaaacaactt agtttttacc atgtgccagg cattgtccct agttgctgac 420
aatacagttg aaaataaaat agacaaaaat cccatctttt gaatcttttg aaccttacat 480
tgggagtgac aggcaaaaac gaggtaaaat cagtaaaata cgtgagacag aacgctaaaa 540
gaaaaaaaaa aggaaagggc tgatttttgt gtcttcccct ccagaatgca agctcccttg 600
aggatacaga tttnggntgt ttttttacta ctgtatctcc tgacaanagg cgcccagtaa 660

cataggtang gcattcgatn ccaatttttn aaaatgagan actaggcagt tac 713

<210> 167
 <211> 714
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(714)
 <223> n is a, g, c or t

<400> 167
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60
 atggcactac attctctggc cttttatcag cactctgaca gctctctcct ttgcttattt 120
 tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg 180
 gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctaccag 240
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggttc tctatcttcc 300
 ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360
 aattcatact gcaaaacaac ttagttttta ccatgtgcca ggcattgtcc ctagtgtgct 420
 acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480
 attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
 agaaaaaaaa gaggaagggt ctgatttttg tgtcttccct ccaaaatgca agctcgttga 600
 ggatacagat ttngtgtgtt ttttanttac tgtatctcct gacaatagcg cccagntcc 660
 atagtaaggc attcgatcca atttttaaaa atggagatac tagggcagtt tact 714

<210> 168
 <211> 792
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(792)
 <223> n is a, g, c or t

<400> 168
 ctttcacgag attctgtctc aaaaaaaaaa aaaaagccaa agtcctcaa atggcctgca 60
 tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt 120
 gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccagg 180
 atctgaaagg ctcacaccct cacctccttc agagggttgc taaaatgtct tctaccag 240

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gaagccttcc ccaaccacca cattaaaaac acacaaccag caccggttct ctatcttcct    300
tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta    360
attcatactg caaaacaact tagtttttac catgtgccag gcattgtccc tagttgctga    420
caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca    480
ttggggagtga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa    540
gaaaaaaaaag aggaaagggc tgatTTTTgt gtcttccctc cagaatgcaa gtccttgag    600
gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt    660
aggcattcga tccaattttt aaaatgtgat actaggcagt tactcagttt ctgggcacat    720
ttnaactttt agacnataat accgattaaa aaaancgggt ncagctaggc tacgatncaa    780
gananaactg tn                                                                792

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<210> 169
<211> 691
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(691)
<223> n is a, g, c or t

```

```

<400> 169
ctacgaacaa ccattggtgag tagaaccatc tggattttcc atcactttca tttaaaagac    60
tctgttgata ttctaggtac tgattccata tatcagatc aacaaatttc tcaaccaagg    120
ggataattgg tttatctggt tgcaattcat tccgtaattt agaaaggaga gaaatagctt    180
tcttttcagc ttccacgcct tcttgcaaaa atacaagaaa aatcaattgt gtgtgtgtct    240
gtgtctgtgt tttgtgtgtc gtgtctatgc aattcctcta gggtaacata tttttacaga    300
cttaagaaga aaagaaaaat gttcaaacta cattatactt ctttaaacaat tacatttaga    360
actcttaaac tgaaaatcaa aaaacacaca cagatctcat atgaacataa tcatgcctta    420
tctatctaag ttctggcctt tctgtgtctt cggatgatcat tactacagag ggaaaggaac    480
ccctgacaga ttttccatgt ctttcatgct tccatacaca ttcttctttc accattgaca    540
ccactagaaa agaaactgtg gcctttctga gggttctttt ggtagctcaa ttttttttn    600
aacttgtttt cactgagtt ctagctaggt gagagatgag atatgctgac atacaaggcg    660
ctncaatatt atctnacatg acaggccaat t                                                                691

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<210> 170
<211> 699
<212> DNA

```

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(699)

<400> 170

```

ctcaaaaaaa aaaaaaaagc caaagtcctc aaaacggcct gcatggcact acattctctg      60
gccctttatc agcactctga cagctctctc ctttgcttat ttgtctctc attctagcct      120
ctggatcttt gcccttgctg ttccttacgc tcttctccca gggatctgaa aggctcacac      180
cctcacctcc ttcagagggt tgctaaaatg tcttctaccc agtgaagcct tccccaacca      240
ccacattaaa aacacacaaac cagcaccggt tctctatctt ccttcacttt gcatttgctc      300
attgtgtaac atcacttaca tacctttaat ttttagttta ttaattcata ctgcaaaaca      360
acttagtttt taccatgtgc caggcattgt ccctagttgc tgacaatata gttgaaaata      420
aaatagacaa aaatcccatc ttttgaatct tttgaacctt acattgggag tgacaggcaa      480
aaacgaggta aatcagtaaa atacgtgaga cagaacgcta aaagaaaaaa aagaggaaaag      540
ggctgatttt tngtgtcttc cctccagaat gcaagctcct ttgaggatac agatttgngt      600
gtttattact actgaatctc cnggacaaat agcgcccagc acatnagtan gccattcnat      660
ccaatttttn aaaatgagat actagggcag tnaactccaa      699

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<210> 171

<211> 767

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(767)

<223> n is a, g, c or t

<400> 171

```

catctcacag agttacatct ttcccttcaa gtaatccttt cgctaaggct gttcttgtgg      60
aattggcaaa gcgatatttg gaagccccta gagggctatg gtgaaaaagg aaatatcttc      120
cgttcaaaac tggaaagaag ctttccgaga aactgctctg tgttctgtga attcctcttt      180
tagaattttc ttcagaactt gtggcacatc attaaacctc cgtcagtgat cacatatctt      240
catccttttg agtcaattta tttttggaaa cagtcaaaag tcactcggag tgacttcagt      300
agaatgaagt gtgtgatcaa attggataaa aacttttttt tttaatcaaa aatgagtaac      360
taaaaaaaac agaagactaa attttctttt tgaggcatgt aaactggctc tgaaagaagt      420
tccaaataat tcaaagatgg ttttagcaat ggcagcactg ctgaaatcca tcagtctctc      480

```

aagggtgactt aaaaggataa atatcattcg gatgcataga gccaatccgg tccaccacct 540
gttttgtctg actcacatgc taagagtggg ttttatattt ttgaatggct gaaaacaaaa 600
gtgaaagaaa agtagtattt tgtgatacat gaaattcaaa tttcagtgtt cattaaataa 660
agnntttctt agaacacagc catgctcatt cttacatatt atttaaggct gcttttcaca 720
ctacaacgac aggnnttcagc agctgcaana aaaaccacat ggcccca 767

<210> 172
<211> 769
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

<400> 172
ctttcacgag attctgtctc aaaaaaaaaa aaaaagccaa agtcctcaaa atggcctgca 60
tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt 120
gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg 180
atctgaaagg ctcacaccct cacctccttc agaggtttgc taaaatgtct tctaccaggt 240
gaagccttcc ccaaccacca cattaaaaac acacaaccag caccggttct ctatcttcct 300
tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta 360
attcatactg caaaacaact tagtttttac catgtgccag gcattgtccc tagttgctga 420
caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca 480
ttggggagtga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa 540
gaaaaaaaag aggaaagggc tgatttttgt gtcttccctc cagaatgcaa gctccttgag 600
gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt 660
aggcattcga tccnattttt taaatgagat actaggcagt tactcagttt nctggggcca 720
tttcaacttt tagacaataa taccgatnag aaaaacggtt acagctagg 769

<210> 173
<211> 769
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

<400> 173

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cagagaacac agnagtcagt ttctcagaaa gcttctttcc agttttgaac ggcaagatat    60
ttccttttttc accatagccc tctatgggct tccaaatata gctttgccaa ttccacaaga    120
acagccttag cgaaaggctt cttgaaggga aatatgtaac tctgtgagat gaattctacg    180
atacatgtaa cattctacga acaaccatgg tgagtagaac catctggatt ttccatcact    240
ttcatttaaa agactctgtt gatattctag gtactgattc catatatcag tatcaacaaa    300
tttctcaacc aaggggataa ttggtttata tgtttgcaat tcattccgta atttagaaaag    360
gagagaaata gctttctttt cagcttcacac gccttcctgc aaaaatacaa gaaaaatcaa    420
ttgtgtgtgt gtctgtgtct gtgtttgtgt gtgcgtgtct atgcaattcc tctagggtaa    480
catattttta cagacttaag aagaaaagaa aaatgttcaa actacattat acttctttaa    540
acattacatt tagaactctt aaactgaaaa tcaaaaaaca cacacagatc tcatatgaac    600
ataatcatgc cttatctatc taagttctgg cctttctgtg tcttcgggtga tcattactac    660
agagggaaag gaaccctga cagattttcc atgtctttca tgcttcata cacattcttt    720
tttcaccatt gacaccactn gaaaagaaac tgtggccttt ctgaggttt    769

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<210> 174

<211> 784

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(784)

<223> n is a, g, c or t

<400> 174

```

cttcaaatgt tgaaaaagag ctgaaatgct gcacagctga atgaaggatc ttctcaaggc    120
tctcctggcg cgagccaatc ccagcctcat gaacgagaga gatcctgaca cccacagatg    180
ggcacctcac agccacatgg agacagagac aggctcgggt accagccacc ctcacagcca    240
cacggggaca ggctcgggtga ccagccaccc tcacagtcac acggggacag cctcgggtgac    300
cagccaccct cacagccaca tgggacaggc tcgggtgacca gccaccctca cagccacacg    360
gggacaggct cggtgaccag ccaccctcac agccacacgg ggacaggctc ggtgaccagc    420
caccctcaca gtcacacggg gacagcctcg gtgaccagcc accctcagag ccacacgggg    480
acaggctcgg tgaccaggca ccctcacagc cacacgggga caggcttgggt gaccagccac    540
cctcacagcc acacggggaa cagctctcgg tgaccagcca ccctnagagt aacatgggga    600
caggctcggg tanccagcca cccctcacag ncacacgggg gacnngggctc ggtgaccagc    660
cnacnctnac agneacaccg gggacagggc tnngtttacc agcccacccc tcacagaccn    720

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caacggggggac aggggtttcgt ngaccagccc acccettaca ntccacacgg nggnacagcc 780
ctcg 784

<210> 175
<211> 733
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(733)
<223> n is a, g, c or t

<400> 175
aatgtgggaa atgcatcatt tgaaacattt taatggagag actagtattt gatataattaa 60
tgtaggttc ctcccagaac ttaattttta aaatttttat ccaaacttat ttactttaat 120
tatcaccatt tattgaatac attaattgaa atagctcagc tcttctgacc tgtggagcaa 180
aggmntgacc ctccaggatct cctggaagct gccctcaact aagcagaact cagaggaaac 240
ttttgactga gaaactgagg tgggtcaaatt gtgctaattgt taaaatacat aaaatagaac 300
atttctttca atcagaacta ctgacactat tacatggcac aggttgccag ttactctgat 360
tagaaatact aaacagaaaa aagaaaacac ttggcttggga tccttaaaga ggtatttacg 420
gaaggtgttg ccaacacagc ccatcccaat gtctggtgag atttcctgtc tgggagaggt 480
ctatgggatc tcacccaaac accacagacc ccagtagcat ttcctggact aatgttcttg 540
tcttttcaca gtgctctgct gatttggctt ttagataacn tggctcttct tcctcttcat 600
aggnatctat accccctgaa gtgtgggtcc ttagactcag ggggcttctt caaaagccct 660
tttggattca gnanaaaaag aancctgggc acttaactgg ggctnaaaga aacacttctn 720
ccgggttccn caa 733

<210> 176
<211> 729
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(729)
<223> n is a, g, c or t

<400> 176
catgtccttt tcagtaacat ggatgtaatt ggaagccatt attctaagcg acattaatgc 60
aggaaaagaa aatccaatac cacatgttct ctctgtataa tcggagctaa acattgggta 120

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cccagggaca caaagatggg aacaatagac attggggatt ccaaaatatg ggatgtaggg      180
aggagggaaa ggatttataa agtgtctatt gggactacg tttagtacct ggggtgctgag      240
atcatttgta ccctaaacgt cagcattatg caacatacca atgtaacaaa cctgcacatg      300
tagactctga atctgaaagt tgaaatactt tttaaaagtc tattatatta tcacacaatg      360
accccataaa caacaacaaa aaaaagtga agtaaaaaaa cgcaaggctt ttagacgtag      420
gaatcagaat gatataaaga aggaaaagag atttatacta atatagaacc tttttagaca      480
tgaattttta aaaaatgata cctagggttat caagttactt ttgtgtccac ctaatattta      540
tacactgtat ccctaaccac aattggctgt attttgaaga cagagccctc aaaggaagta      600
attcagggttn tgggtgtccct ataaggagga gaacactagn agnatctcag cttctctcca      660
ccccaccccc aacccccaca aaaacatgtt aaagaaagnc tttatnttgn gggacacagt      720
nggagaaaaa                                     729

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<210> 177
<211> 679
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(679)
<223> n is a, g, c or t

```

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<400> 177
catgcaaggt caggtgcagg catctcttcc aatagggcag tgtctaccag gtagggcttt      60
tctcctctta gaatcattna tggaaatata attcacacaa cataaaattc accctttaaa      120
actatactac acacacacac acacacacac acacacgaat aaaccatata ccattagcag      180
ttattcaaca cactctgccc ctttgacccc tggaaataat cactaatcta ctggctggta      240
ttatggattt gcttattctg gacaaatcat agaaattgaa tcattaaaca tttgggttatt      300
ttgaatctat cttctttcac ttggcataat gtttgcaagg tttatccatg ttgcagcaag      360
taccaatact cattcctttt tatgcttcca taatattcca tggatataat ataattttag      420
tcaattttta agtcggtgaa catttacact gtttctcctt tttagctatt atgaataatc      480
ttgctatgaa tattcatgta caagtttttg cataaacacg tttncaatc tctattatgc      540
acctagaagt ggaattggta ggtcatatgy taattctatg ntnaactttt gngaatatat      600
gccaaactat tttccaaagc aactgcaccc atttngtatt accaccatta aggnataaaa      660
ngttcctact ttcttcaca                                     679

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<210> 178

<211> 737
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(737)
<223> n is a, g, c or t

<400> 178
ctttcataat gaaaagaaaa aaatgaatth caactagtat cgatttttcg gtgtgtgggg 60
gcagggcatt taagggtatt atttcctagt aatgatcact tagattctaa gccttaaaca 120
tgattcaaat gcagcagaaa tcaggaaaaga agcaacagat acggtgggtgc atatcgaatg 180
tctagactac aaggcaaaac ccaaatacca aagaagcatc catgtgtcaa accagcataa 240
tttctaagct atgcctgggg ccacatacaa aaaaaaaaaa aaaaagggtta gtttgaaaga 300
aaaatctagg aggggtaacc agaagggtcaa cccagttca caggaactgg gaagaagcta 360
gccgttacc tgtgacatct tctgagcag cttcctccgc agccagctcc ccagcctcct 420
tacaatgttt ccaaaaggcc caactcccta aacatttgc tcttcaaggt catcctaaga 480
taaggcagtg aataaccacc aaacactgag tcacggatac ctttcggcta aaaaagatcc 540
cccttcccaa aatcattaca taaatacttt aaatgccaa agggttttct ccggaactcc 600
accagaaact ccagnactt taatttagat tgggcaacta aatgtgttca anttttgcgc 660
cataaaatat taaaggcttt tcaggctctg caantncagt tcaaacagg tgctttcagt 720
gtacgctgaa taacagg 737

<210> 179
<211> 759
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(759)
<223> n is a, g, c or t

<400> 179
cagatttttc tttagaatt ttgtttattg caataggatt atcaaagtaa aaattaaaaa 60
gtaatgaaaa aattaaaaaa ataattttgt agctaccctt cctataaaac ttatccagat 120
tacttcttga cctatacttt gagagcagag gaaatctagc tacattaact cagtagctct 180
gcaacttcta ggtaatttct tacctgaaca gtatatccta agtactgtaa ttcctgcatt 240
gcttgacat ttgagtttat tattccatcc ctgtattaca ataaatattc tttacataaa 300
ctttcaagag aaaaagcatt caaggatat gtgtgtgtac acacttatat atatgtgtat 360

atatactcct gtaaaccata attggagttt aaaaaatata tggatattgc aattttctct 420
 tctttctctc tgtctctctc tctctctctc tctctctctc tctctctctc tttcgatgga 480
 gtcttgctct gtcacccagg ttggagtgc gtggtgtgat ttcagcttac tgcaacctcc 540
 aactcctggg ttcaagtgat tctcctgcct cagactccca agtagctagg actacaggtg 600
 cgtgccacca tgcccggtta atttttttgt attttttagta gagatggggg ttcaccatgc 660
 tgnccagact gntcttgaac tccctgacct tctgatccac ccgcctcgtc ctcnaagtg 720
 ctgggataca ggncatgagc caccaccccc gccggtatt 759

<210> 180
 <211> 770
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(770)
 <223> n is a, g, c or t

<400> 180
 cagcttttat atatgctgag ttcaagacac ataagtacat atagataant aatgtacact 60
 tcttctgtaa gaagacatat aagactgtaa tccatgagag agggaggtct aagatgacat 120
 gtttgggaat ccttttatatg gacatgatag atgaagccaa agagaacaat gaaatgattc 180
 atgttgagtt atttgacatt ttaaaaagta tataagtatt ttaatagtgt gaccatttgt 240
 gtctggaaat tttgaaaagc acaaatgatct acaatgattt atttatctct atactgatct 300
 gtaggaagtt tttggcatgg gaaattgtgc taatgagtat ttggaaacaa gtgtatgaag 360
 taagggttta caagatcatt agactttcat tttgcagact caatcagatc tgttcactat 420
 agtctcctgt tggcataatt ggtttcctga ggacttatta cctgtagatg cacaattttt 480
 cattccaaca atgttctgca ttctttttgg actttcctgt cttgaggatc tctttaaaga 540
 gctaaaacct caggaaacttc ttctacttgt ttctttaaag tcaggatgag agacagaata 600
 aggcattccag ccatgatggt ttttccccag gttcttctct catgctaagc cttttatggt 660
 acgatgtgcc tctcaaagga gaatgcagat ctaatactat tgcaccactc tgaaagaagt 720
 atgaggagaa ggcanaagag ctatgaaaag aaaaacatcc tgatcttttt 770

<210> 181
 <211> 706
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(706)
 <223> n is a, g, c or t

<400> 181
 ctttcatgcc tagtaaagag tggggccttg cctggagagg gaggcctcat gggccagata 60
 agggagatgc tggcccatct gggcacgcat gtgcccgtag gctttccctg tcgagatgat 120
 caactggaaa ggcagagaat gcggcctgga ggctcagaaa catccttgaa gccatatccc 180
 caggctcctag tcctaactgc cactcttttc tttttttgaa atgggggtctt gctatgttgc 240
 tcaggctgga ctccaactcc tgggcttaag cgcttcctcct gcctcaactg cccaagcagc 300
 cacaaaccac acctggcctc ttctgccac ttctagctta gcagggtggct tcatctgtat 360
 acggggatga cgtgactgct tgggggaatg agctgagccc ttggtggaat catggttcat 420
 gcaagaggtc tccggcaaaa tgctccaggc ttggagtctg ctgggcgctt ctaccctga 480
 caatccgttt acttaccacc accctctgtt cagacagga agttctttcc atcaggatta 540
 tagcgaggat tggcttctcat ggcacccttg gcacccgagc acgtgttgtt ggagctgttc 600
 tacgagccag gacacaccag ggaacggttn cccgcaataa acaccgtct ctccctcgta 660
 ctcaagttct tcgggggttg aacattctga gagcttgctc ttcat 706

<210> 182
 <211> 740
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(740)
 <223> n is a, g, c or t

<400> 182
 cngngnctcg atcgttcctc ccacctcagc ctcccaaagt gctgtgttac aggtgggagc 60
 cactagacc cagctgaatta tggattttta aggctgcttt atgtcaaaca ttgcgggttc 120
 ttttaatat gttttccaga ttttaagattt ttttctttta agctttgtat aatttatagt 180
 aatttggtaa agtacttttg aaaacaaaaa tgaaaacatt tgcttttctt ctctacctga 240
 acctccaga atttagaagc aatttatgat tattcttatt ttacagcaa catggttatt 300
 tgcatagggt cagtaagaat ctgttctctg tccaggcaca gtggctcaca cctataatcc 360
 cagaactttg ggaggctgag gcaggcagat cacttgagat caggagtca agactagcct 420
 ggccaacatg gcgaaccct gtctctaccg aaaatacaaa aattagcctg gcgtgttggg 480
 catgtgcctg gaatcccagc tactagggag gctgagtcag gagaatcact tgaacctgcg 540

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agggtggaggt tgctgtaagc tgagattgta ccactgcact ccagcctggg tgacagagtg      600
agattttgtc tcaaaaaaaaa aaggaggggcc aggcatagtg gctcatgcct gtaattccag      660
cactttggga gaccangggg agcgaatcac anggtcagtt cgagggtgact ntaggganaa      720
aattatgttt naatagaaaa                                     740

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<210> 183
<211> 720
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(720)
<223> n is a, g, c or t

```

```

<400> 183
aaacagtaaa aaataaggaa ttttactttc tctggggctc ccaggctctc tggttgggtc      60
agggcccaag tggagcaggg aagaaggggc cactctttct gaagtctccc tgcataaatg      120
aaaataacag ttgagtggca gtcacacact tagaagcaaa tcattctgat ttgccttct      180
agagcagaga tgtctccctt aagatccatt ttaccccagc agaaaaagcc cgggttgtct      240
ggattgtagc aacgctgttt tgacagaaag ccctatgatt tttctcaca acttcctaa      300
ggatgctatc tttcagctac acatacttag attatttctt ctccctcacc aactcaatct      360
aatgttgcta aggggttcag tacttttctt ctgctgctta cctcgtccca acccccaagt      420
tctttcccaa attccagcag ctgggaccag tctctgggac agagcagaaa taacatggaa      480
attgggggta ggggttaaaca catctatcag tctaggaaca ggtagaaaag caacaccccc      540
gtgactacaa gtttggtagt gggcaacaat tttcttatcc atcatgggtg gtggtgtggg      600
tagtnattga gcataanttt atttgtagag gtgaatttgt ttactgggct ntnaaggggc      660
acatggaggc tgtccaagga aaganattcn ataatnaatg gaaatttatt ataatttaat      720

```

```

<210> 184
<211> 775
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(775)
<223> n is a, g, c or t

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```

annnnactna nnnnnnnnat cggtcnnttn nnttgggggg naanccagta cttcaaaact      60
ttgtattatt taataaatga tactgactag ttggctaaac attgaacaa aagataaatc      120

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tccaaaccat tctaccacc aaaataaatt ctagaaatga acaaagattt caaagtaaga 180
agtaatccac aaaagtacgg aagaaaacaa tcttaaattg gagaaggact ttctaaacat 240
ggcaccaaag gttagaaacca aaaggaatca cttgcagggt tcatcacata aagattttta 300
aattttctata catccaaagc actacaatgt tcagctcaag atggcagggt aggcacattt 360
gcctttcatc tttagagaac catttaaata aaaagacgga ggtacaatga ggaaaaactg 420
taacagggaa gagacgggct ggaacgacag gaagcagatg agccagctgg gagatgaacc 480
agctgaaaga gctgcagtgg agatgaaagc ctgtcctgtg canactgtgg aggaaggagt 540
gaaagacccc acctgtaggt ttggcaagct agctgaggat cgttncncat gattgaacaa 600
natggattgc acnctgggtt tcnngccnnt tgggtggana ggctnttnnn ntttnantgg 660
nccaacanac antnnntgt ttnatncnc cnnntncng tnnnnnnan gggcncncn 720
ttttnttnn ananccacct nnnnnnncc cnnatnaact nnnnncnang nnnnn 775

<210> 185
<211> 400
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(400)
<223> n is a, g, c or t

<400> 185
tttttcccg ngggngnnnn nnnnnnnnn nnnnnnncc ccccccttn nnnnttggg 60
ggggggaaan ncccccccc ctttnnnnn ttttnnnng nnnnngnnac aggtttttt 120
ncngggggat nntnttance ccannnttt nnnccagng gnnnnccann nnnccagcnn 180
ggnggnannn tgctnnctg cncgnnncca gcccgctct tnnctgnta cagnnnnntc 240
ctnattgnac ctccgctnt ntatntaaat ggntctctaa agangaaagg caaatntttt 300
tttctgcca ttttgagcng aacattgng ngctnnggat gnatagaaat tntaaaant 360
tnntgtgang aaaccngcaa gtgntttttt tnnngnncct 400

<210> 186
<211> 951
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(951)
<223> n is a, g, c or t

<400> 186
 ccgccnggtg ntgggaaaga cnnnggacgc ttcagaccac aggnaggtac catcctggaa 60
 cctggaatct ggaacctcag gggctgacct ggcactgggt gggcctggaa cctgtatctg 120
 cagcccagaa gcagggtctg caggtgcaag cctgatgcca ggctgcaggg gacagccng 180
 agcnggtttt tnttgaggca ggggntgata angccagcag gcccaaagca aagnctaggg 240
 cnnatntntg tctctaccc ccatgcngag gatacctnnn ttnaagctgc ggagccngag 300
 gaaggagggg ggcgcangca agagaatgtc anaactancc ttncnnacct nctncangnc 360
 nacctccagg ngctgtaanc actcactagg anaccettaa ggncnnactg aaaggagcnt 420
 ccctangagn gatggnagca aaaaananga nacgacactn cgactgcnnng gngacgtgca 480
 acntggaaag actctgnncc ctncancacc tcgggnanac tatnacaaag angnccccca 540
 ncacctncaan aatgaaagna aangtgancg ngcnanacca acnncgacnn ccctnggccca 600
 agagaacacc aataacnaga ntagganatc caaaagcggn aaanacnaca gngctatnng 660
 gaatgcncaa gccacatnn cttgcantgg nncaacagnt gnaatcnaaa nctacnnccn 720
 cnatacactg gagagacaan naccnagcnc cantaaagcg nnaaaaanga gaaaacgnaa 780
 aaaancgcg c anngnngcng ncnaatngcc cnnacenta cccctccnnan aaaaannaat 840
 cngaacctg gnnacgacnn ncnaagnggc ncaancnc cncaggcgnc tcnnccnct 900
 gccacnanca cccngagcc ncnnagagn caccngcctn acncacccan c 951

<211> 450
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(450)
 <223> n is a, g, c or t

<400> 187
 tntctntttn ggggtnnnan nnnnnnnnnn anntccncca atnnnnntgg gggggaannc 60
 ctggttttct gcactctccc tcttttccac tcatgtcgcc aggtctccca aatgttccct 120
 gactattctt tccctttttt gtgcccacct gtgcccagg cacagcatgt gacctagtcc 180
 tgggagtccg cggtggcaga actgcaggcc gttggggcct ccaagtagac catgcaagtt 240
 tcacagccat attnctctga tatcagaagc taaggagtgc tgctggcca gtactaggat 300
 ggggggtccgn ctgggaacac tgggtgatgt aggctttttg cttacagnnc cctccctctn 360
 tccccctnca gnnngctnga tncacaacca tncctgact ntntntnctn ntnnnnncac 420
 ccaactgcat ncnanacaca nncngngact 450

<210> 188
 <211> 338
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(338)
 <223> n is a, g, c or t

<400> 188
 tncncttnt ggnggannna nncnnnnnnn nnnntccnc ctnnntggg gggggaannc 60
 gnncacntnc nntttangaa agagacgacg cttncgagga agaaggtttn tgggacgcgg 120
 gactgggnag agctccagag cccagcagc ccggtcaag gnccctgcg cataggcgcc 180
 ccaccngac gncagggacg cgactnccgn gangccccgc gcgccgnng anccagggc 240
 cgggcnnaga ctgngatcnn ggagnngccc ngngccnnnc ngacggngcg nnnngnggn 300
 cnngggcgcg ggcnnngnga nnggacagnc nggagcnt 338

<210> 189
 <211> 936
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(936)
 <223> n is a, g, c or t

<400> 189
 ttttnngggg gaannnnnnn ngngtangn rnnnnnnccn ccgcggttnn nccttggggg 60
 gggaannncc nnnccangtn nctttttcat gnaaagnna cgacgntctc cgaggaagaa 120
 ggctccggga cgcgggactg ggtagagctc cagagcccca gcagcccggc tcaaggctcc 180
 ctgcgcatag gcgccccacc gtgacgtcag ggacgcgact cccgcgatgc cccgcgcgcc 240
 gtctgatccc aggcgcgggc tcanntttt atctcggagt tccctgcgc cttcctgacg 300
 gtgcgttctg gcggcctcgg gcgcgggctc tgcgatcgga cagcctggag cctttggcct 360
 cgatttacat gggaggcccc tcgaaacagg gcacgtcact tgccccgggt cacctgcgga 420
 cggggagact ctcggttga ctccaaggcc tgacattccc ctccggtttt caccgaggag 480
 gatgaggatg ttgtcaggag ctgcggcaag gctggaggag cttgcgttgn gtccaccnc 540
 ctctgnacag gccttagcat ncaccncag tttctccctt gactntgaa ccnaactcc 600
 ttacccccgc aagtnnennc cctgtttnga ttgctgaaac tgcaagtgc ggaagantaa 660
 aatgtttgcc naagcntnat gcttnanggn ggntgccngg gtataaggtc angggttggg 720

```

ggccctttnnc cctgnnggggt nggcnttaag ntaaccagg gnncntggca nttnantnt 780
attcaanana tgccanggnn ntccgnntnn aanggnnttt tnnanaaaat nnttncctt 840
nttannctnt annccnnagg gaaanccntn gggctcttgtt tngccctgna aanacnatna 900
aaggggtaat nccccncnct tnaatntnnn gncncc 936

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<210> 190
<211> 936
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(936)
<223> n is a, g, c or t

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```

<400> 190
ttttttnngng gannncnnnn gtttntngnn ncccccccc ccatnnnttt nggggggggaa 60
nncccnnnca cgtcctcntn atgaaagaga cgacgcctcc gagaagaagg ctctgggtac 120
gcgggactgg gtagagctcc agagccccag cagcccggt caaggtcccc tgcgcatagg 180
cgccccaccg tgacgtcagg gacgcgactc ccgcgatgcc ccgcgcgcgg tctgatccca 240
ggcgcggggt cagantnna tctcggagtt cccctgcgcc ttcctgacgg tgcgttctgg 300
cggcctcggg cgcgggctct gcgatcggac agcctggagc ctttggcctc gatattacatg 360
ggaggccct cgaaacaggg cacgtcactt gccccggtc acctgcggac ggggagactc 420
tcgggttgac tccaaggcct gacattcccc tccggttttc accgaggagg atgaggatgt 480
tgtcaggagc tgcggcaagg ctggaggagc ttgcgttggg tccaccgcc tctggacagg 540
ccttagcatt caccgcagt ttctccctga ctttgaacct aaactcccta cccccgcaag 600
tccttcctg ttttgattgc tgaactgcaa gtgacggaag aattaagtgt tggccgaaag 660
ctgatgttc agggggtgca ggntagaggt caggggtggg ggcctngcct tnggngngc 720
atantgtanc ccanggtcn gactgantn ttnnaggaat gcanggaatn gnatannang 780
gtntaanaa antntcccc tannaactga taccnnagna accntngggc tgnntgancn 840
tgaaaaaccc annagggtaa ngcctnnctt atnngggccc cnntntcnag annaaangcc 900
ctgggggttc anngaaaacc cnnnnanaaa ntntgg 936

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<210> 191
<211> 951
<212> DNA
<213> Cercopithecus aethiops

```

<220>
 <221> misc_feature
 <222> (1)..(951)
 <223> n is a, g, c or t

<400> 191
 ttttttngng gancnnncng gttgttggnnc cntcccgccg attcccttgg gggggnaacc 60
 ccnnncang tncctnttna tgaaagagac gacgcntccg agaagaaggc tctgggacgc 120
 gggactgggt agagctccag agccccagca gcccggtca aggtcccctg cgcacatggcg 180
 ccccaccgtg acgtcaggga cgcgactccc gngatgcccc gcgcgcgctc tgatcccagg 240
 cgcggggtca nanttnnnc tccggagtcc cctgcgcctt cctgacgggtg cgttctggcg 300
 gcctcggggc cgggctctgc gatcggacag cctggagcct ttggcctcga tttacatggg 360
 agggccctcg aaacagggca cgtcacttgc ccccggtcac ctgcggacgg ggagactctc 420
 ggggttgactc caaggcctga cattccccctc cggttttcac cgaggaggat gaggatgttg 480
 tcaggagctg cggcaaggct ggaggagctt gcgttgggtc caccgcctc tggacaggcc 540
 ttagcattca cccgcagttt ctccctgact ttgaacccaa actccctacc cccgcaagtc 600
 cttccctggt tgattgctga actgcaagt acggaagaat taagtgttg cgaaagctga 660
 tgcttcaggg gntgcaggg tagaggctag ggggtggggc ctgccttgt gngtgcata 720
 tgtagcccag ggtcntggca ctgattntta ttaggaatgc agggantng attagatggg 780
 ttcttagaaa atatcccctn tgnantgnt acctgagnaa ccgctgggct ggcatnacct 840
 tgnaaaacc agaanggtta nngcccttc ttantngtg cccnattttt tcaggacnaa 900
 anggccntg gnttttcaat gnaatcncnt ttgcncaaan nnctggttc t 951

<210> 192
 <211> 938
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(938)
 <223> n is a, g, c or t

<400> 192
 ttcnnggntc ttntgntan attttcccc ccattttttg ggggggaanc cnacncanca 60
 aaaggtagaa attattgata aantntaaat gttacaaact gcngctaaaa gaagcaaaag 120
 agaacatgct gtatgatcct tttttttttt tttttttttt tttttttgag gcggagtctc 180
 actcttggtg cccaggctgg agtacaatgg cacaatctcg gctcaccaca acctctgcct 240
 cnnnttttca agcaattttt ntntctann ctccctagta gctgggatta taggcatgtg 300

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ccaccaggcc cagetaattt tgtattttta gtagagacgg ggttttctcca tgttggtcag      360
gctggtcttg aactcccgac ctcagggtgat ccaaccgcct cggcctccca aagtgtctggg      420
attacagacg tgagccactg tgcccggcaa tcttttttct taattttaaa ttttttagag      480
acaaagtctg gcttttctag tnccaggctg gagggcagtg gagccatcct ggctcactgc      540
anccttttnc tcccaggctc aagccatcct nctaccttaa ncttcctgag tngctggnaa      600
ctacaggtag acaccacat gtcagnctaa tttttttttt tttttttttt ttgaaaccna      660
attttttctt tgttcacccc tnntgganan ncaggngna nnanctctnn ccnctcnac      720
cccttacnnc naagnncaat atnaantatc nncctacnnn ccnagntct tnnntttta      780
annnannttn tatttttntt ntttatantt tacctnnntn tttctnnntn ctanaccctn      840
ntnactnnt nnactantct tttccacnt attcttctct ncnctntnc tnatatcncn      900
nncnnnctc tctctntnc ttctttnttt ctnnnatn      938

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<210> 193
<211> 804
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(804)
<223> n is a, g, c or t

```

```

<400> 193
tntngggggt nnaaaacnt tncnnacata atcgccncaa tacaanttgg gnggggaaaa      60
annctgnntc attctcctt gnacccatct ccatgccgtg naagcatctc ctncctggac      120
ttgcactatc tgggccata gcccttgctt attcttaa atggagtact ctgacttgca      180
ttgtggggaa gggatatacct ggggcacagt cctctgggat ggacacttcc ataggaaggg      240
gcagttatac ttggacttat gtctcctac actctcatcc agaaccatcc accagaagc      300
aggagtgtgt tcttttagaa accagccggc ccaatcagcc cattttatag gtgaaggcag      360
tgaagcccag agagataaag catcttgtcc aagggtcacag agccagacct agactaggct      420
gcctggctcc tagttcaggg ctcatccac cctagccggc ttctggctag acagaatcta      480
cccatcctgg ccagactct ctgggtggaa gtcagggatg cagnggtcag gatgggcatc      540
agagccagca ggcctgagc acggnctacc caagtgaac atgaacttcc taaactccag      600
nggaagttag aaatggcana ttgatcagng ctaatgagct taaaacaccc agggattaaa      660
aaaaaaaaca tgaanaagct ntacttnaag cataaatntg ntnaacanaa agganaccng      720
gctncncnt ntntnanann nacnnnttg aggctnaggg ggnnngnca tnnngggngn      780

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ganattngnn ttngnaaggg gnnt

804

<210> 194
 <211> 560
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(560)
 <223> n is a, g, c or t

<400> 194
 ttctantnn nnnngttnna ancannnnnn ncatnntcgn cncatnnnnn ttgggagggg 60
 aannnaatna ataatacaan ttagnaattg aatttagaat ttcatttatg aataaaaagg 120
 ctgggaggaa acacacccca accgacacag tggatgcatg aggataagac tatgagcaga 180
 ttttgttctt ccttttcacc gtctgtattt tccatcaatt atttgtatga ttaaaatcaa 240
 tcatttcaga caagagggac attgtgagct atctgtgaga aatgtcttct atctgtttcc 300
 agatagaagg ggctccagct cggtttgggg aaagtcccaa tgccattctc ttaaccaaga 360
 ggtttcctac ctcatctaata gtggagattc tacttaccg ggaagactcc cctcctgtta 420
 cctcaagtct cgagccggcc tccagactt ctgcctnctn ctaaccacag cctgcctggg 480
 tgcaggncgg ngggaaagga gggcatangg ggctgnatnc cgnanaggcc ctnnactcc 540
 tngactnang cagggnnctg 560

<210> 195
 <211> 977
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(977)
 <223> n is a, g, c or t

<400> 195
 cnnccccng gntnccccng ggnnnnnnnn nnnncccccc ccnanncttt gggggggaan 60
 nncnnncctt tngngnatt gnnnggnana annngtnct tccnnaatag natngggcng 120
 canttcaact ncgctaatta acggaacagc aggctngnaa ttctgacaac agcaggacac 180
 aaanggggcn gggatcagca ctgaatgccg gcgaagcatg ccccccccc ttaagaagaa 240
 gcacaacacc cagcaccac attnnntntn gggncaggtc catgaaggng cnaccctnga 300
 tttagttana ngcctnccc tgcagcaact ccaagggcnc agggttttta aaatgncnc 360
 tcaggccttc ttnagaggna gcaagccngc cccaactggc ctttttcnna aaaaagang 420

```

aacacaggnc t gngattggte nagagcagga nncgcccagc ccnttnggct ccccngggcc 480
acacngnaag aaaaagaatn gnnttgacc acacagaaaa cacaccaana ctaangacag 540
ctgaaaagct caaaaaaaaa atcgcnaaaa aatccctcaa tgctcnaaga agtcncaaaa 600
nncgccgngn gacngnnaca cagctnccng gccngcanga cncngggggn ncacaggngn 660
cnacacccag gaccagnagn taatatacna aaagggtaac aanaaaancc ctaataccaa 720
aaangcnatg anaatggaag cnnnacntcc tncaaaagac aagccctang gaaancntcn 780
cncnacccnn nccccaacn ggcanncggg cccccacca aaaggggggn nccgccccgg 840
aannnaaaan ccnacnnngg ggaaaaanng accnnaancc ngaaanngtc tatancccca 900
cngnccnaaa acctcccang ncaatnaccc cncctccta aaaggntagg annaanaacn 960
ngnggcaaag ncnncca 977

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<210> 196
<211> 868
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(868)
<223> n is a, g, c or t

```

```

<400> 196
gaannccnnc nnaaaaaacn nnnnncccc nccccatann ncttgggggg gaaannnccc 60
ccccacaagn natantnagn aggnaggaaa acacanttaa tatatctcac tagcnctcat 120
ttccctcccc caccctcatc ccactccact gctaagagag agaaatnna gcactgctat 180
cctgtntat tatacatntt cccttnngag tnaaggattn naagattnng aaagtaacag 240
aatagaaacc aaaagtnnta ctcaactncc aatttggctt aaaaagagag aaataatnat 300
tattncctat gnnacccaaa actnattctg nnaataacag ntataattat atattcaaan 360
naataaatga agatcgcaa aatcacctna atataatngn nagcagctaa agaacaaaaa 420
tnnnnnncat nngctnctat aagnagacat cacatganna ctntatnga ccagnaagaa 480
actagnaaaa ncaggcagnc acccaccatn cnnnnctaac annnnnnnc nnannctatn 540
caaccnnnnc ggnatanncn naagaagcca aatcaagaaa nnagaccnnc atgcctaaaa 600
aaaaanngng nnatcnnaan acatcangaa caggaaccng nngnanataa cacaggmann 660
caaagcnnna ncncaannn cnagaaccn naaacanaaa ggcagcnnan anncaagann 720
agaaacngaa nncacanaac acanagcann nncncanaaa gcnnnnnnca nnnnngaacg 780
aagaaannnc nnnnnaccaa aggccncaag ggcnnncaa nccnnngcc aannnaaaaa 840

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aaaccnanca aaggcncnng anggaaaa

868

<210> 197
 <211> 260
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(260)
 <223> n is a, g, c or t

<400> 197
 ttttcnggng gannnnnnnn nnnnnnnnn nccnccccn tnnnttggg ggggaaannc 60
 nnnncacang nnatnttngn ggaggaaaac acatttaata nantcatta gccctcattt 120
 ccctccccc ccctcatccc actccacnng taagagagag aaatnncagc actgntatcc 180
 tgnnnnatna tacatttncc ctnnngagtn aaggatnnna agatnnngaa agnaacagaa 240
 nagaaaccaa atnttttttt 260

<210> 198
 <211> 901
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(901)
 <223> n is a, g, c or t

<400> 198
 ggganancnn agnngnaana nnccaacccc gccaanatnt anggggggan actntcacaa 60
 gtatacaaga ggaggaaaac acaattaata tatctcacta gcattcattt ccctccccc 120
 ccctcatccc actccactgc taagagagag aaatttnggc actgctatcc tgtntatna 180
 tacatnttcc cttttgagtn aaggatttna agattntgaa agtaacagaa tagaaaccaa 240
 aagtttntct aactnccaan nnggctaaaa agagagaaat aatnattatt tcctatgna 300
 cccaaaactn annngnnaa taacagntat aattatatat ncaaataat aatgaagan 360
 cgccaaaatc accttaatat aattgncagc agctaaagaa caaaaanncn ncncannngc 420
 nncnataagn anacatcaca tgatnactnc tatngaccag naagaaacta gnaaaancag 480
 gcagnacccc acccancnnc nntaacatt cnnnnnnna nncnanccaa cctnnnncgg 540
 natatncnna agaagccaaa ncaagaaaan nagaccnnc ngccnaaaaa aaaacngngn 600
 nancnnaaac atcangaaca ggaaaccagn ngnaaaataa cacagggnat ncaaaagcnn 660

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tanccggcan nnnnccaaaa acccctaaac anaaaaggcn gncccagaac ccangaaana 720
gaaaaccnga aanncccngg nnaancccg gancnncccc caatccacaa ccccccgna 780
naancncccn aaaccancc aaaacanaaa acccngnggc naaaaaggcn ccccnaaaaa 840
aanggncccc cggnccggcg gncgaacncc cnagggncan nannggggng nagncaaaaa 900
a 901

<210> 199
<211> 885
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(885)
<223> n is a, g, c or t

<400> 199
ttttttnggn ggnttttnnc nnttttnntc nnnnnncccc cccgattnnn nttnnggggg 60
aaannnccnn nccanaagnn atnttagnag gaggaaca canttaatat atctcactag 120
cattcatttc cctccccac cctcatccca ctccactgct aagagagaga aatttcagca 180
ctgctatcct gttttattat acattttccc ttttgagtta aggatttta gattttgaaa 240
gtaacagaat agaaacaaa attttntca acttccaatt tggctnaaaa agagagaaat 300
aattattatt tcctatgta cccaaaactt attctgta taacagttat nattatatat 360
tcaaattaat aatgaagat cgccaaaatc accttaatat aattgttagc agctaaagaa 420
caaaaatttt tttcatttgc tttctataagt agacatcaca tgattacttc tattgaccag 480
taagaaacta gtaaaatcag gcagtcaccc accattcttt tctaacttc ttttncttat 540
tctatncaac ctttncngta tattcttaan aagccaaatc aanaaatnan accttcatgc 600
ctaaaataaa attgtgntat cttatacatn atgaacagga acctgtngta tataacacaa 660
nntatnncaa agctttatcn cantttctan aacccttaaa caaaaangca nntcanatt 720
nnaanattan aaaactnaat tctggaccca antgtanatt aactctnnan acattttttn 780
gtgnattaan naaaaactgg nnnccatcc ttaacttta naggtcancc caaanttnn 840
nnanaacaan ncctnnnnan aancaantta tatnaacca nctan 885

<210> 200
<211> 941
<212> DNA
<213> Cercopithecus aethiops

<220>

<221> misc_feature
 <222> (1)..(941)
 <223> n i s a , g , c o r t

<400> 200
 ttttnggggg anntanang nnnnnnnnnn nncnngnnn nnattggggg gaaannnccn 60
 nncttngnat ttagaggagg aaaacacntt taatggatct tattagcttc atttcctcc 120
 cccaccctca tccactcca cngntaagag agagaaattt cagcactgct atcctgtttt 180
 atnatacatt ttcctttttg agtnaaggat nntaagattn ngaaagtaac agaanagaaa 240
 ccaanntttt ttttcaactg gnaattnggc tcaaaaagag agaaataatt atnatntcct 300
 atgttaccca aaactnatcc tgnaataac agttatnttt atatattcaa attaataaat 360
 gaagatcgcc aaaatcacct taatataatn gncagcanan aaagaacaaa aatnctttca 420
 nncngcttna ataangnga catcnccatg atcacctnct attgaccagn aagnaaacta 480
 gnnnaatna ggcnanncac ncacnanann nannnaanc accannnnna cnaannncna 540
 ttcaacannt nannggnana ntncnnaat aagccnaaat aanananann gcccnnan 600
 gcctaannan nancgaggna atgcnnnncc caannttnaa caggnatncc nggcagnnt 660
 tntaacanng annatttcan angnnnnanc cggaataact nnnanaannc cnannaaann 720
 naaagggnan tcnnaatnca angttnaana aaangnaatn cncnnnnnn antantaaat 780
 aangncnna ntannannnn nctancatcn cncncnatgc acnnnnnaaa ntnnnnntn 840
 acnnncnnc nngnnaaan nttnaangga nncnnnnntn ancacannnn cncannaang 900
 nnnnnnaana nccacaannc aacacatnan caancacnaa t 941

<210> 201
 <211> 886
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(886)
 <223> n i s a , g , c o r t

<400> 201
 ttttccnng gntnnnnnt nnnnnnnnn nntcccccc catnnnttt gggggggaaa 60
 ancacagnaa cacagngttt nngnnctcag naaagctttt ttccagtttt gaacgtaaga 120
 tatttccttt ttcaccatat ccctctatgg gttccaaat atccctttgc caattccaca 180
 agaacagcct tagcgaaagg cttcttgaag ggaagatgt aactctgtga gatgaattca 240
 cagaacacaa agcagttttt ttagaaagct tctttctagt tttgatctga gaatatttcc 300
 cttttcacca tagacctcta tgggcttcca aatatcacgt tggaaatttc acaagaacag 360

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tgtagcgaa aagcttcttg agggaaaagc tataactctg tgagatgaat tctacgatac 420
atgtaacatt ctacgaacaa ccatgggtgag tagaaccatc tggattttcc atcactttca 480
tttaaaagac tctgttgata ttctaggtac tgattccata tatcantatc aacaaatttc 540
tcaaccaagg ggataattgg ttnatctgnt tgcaaantca ttccgtnatt tnanaaaagg 600
agagaaaata gctttctntt cancttncca cgccttnccct gccaaaaatn ccaanaaaaa 660
ancaatngng nngnggngcc ncnntnntg nngnttngng tgthcentgn nctntccnan 720
tcccnntnag ggnnaacnaa tttttncnga ctttaanaaa naaaanaaaa aanngnncaa 780
accacnttnn aaactnnttt aaanntncca tnnnaaacct taaancnaa aaccaaataa 840
anccccacn ancnnnnnnn nanananann nnnccntan ttnttt 886

```

<210> 202
 <211> 925
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(925)
 <223> n is a, g, c or t

```

<400> 202
tttnttgng gannnctnnt nnnnnnttn nccccnccct annncttngg ggggaannnn 60
cnccccactt agnatTTTTT ncncaaaaaa aaaaaaatag ccaaagtcct caaaacggcc 120
tgcatggcac tacattctct ggccctttat cagcactctg acagctctct cctttgctta 180
ttttgctcct cattctagcc tctggatctt tgcccttgct gttccttaag ctcttctccc 240
agggatctga aanntTTTTT tccctcacct ccttcagagg tttgctaaaa tgtcttctac 300
ccagngaagc cttccccaac caccacatta aaaacacaca accntttccc gttctctatc 360
ttccttcaact tngcatatgt ccattgngta acatcactta cataccttna attntnagct 420
natnaatnca tactncaaaa caccttatnt nttaccatgt nccaagcatt gncccntant 480
tgcttnacan tacancncna anatnaaatt cnacanaaaa tcccatnctt tttgaatntt 540
tttgaacctt acattngnaa gttnncannca aaatccnang ttaaancata aaaatncccn 600
tgnanacnna acccctnaaa naaanaaaat angaaganag gggcctgaat tnnngngcnc 660
tttccctccc caaantncan acntcctngn angnaaccnn atctnnnnng nnnntnnntc 720
actnccgtnt nttcccgaca anaancnccc cnnnccctn ntnggccctt ccatnccnat 780
tnttnaaana ttaaaanccc ccncnctcn ctaanttnct ngggncnctt ttcaaacttt 840
tnaacnaann anncccnccc nnnaaaaach ncnncnccc tnnngnnccc anncaaatc 900

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atccnncntc nntcctctnt ctccn

925

<210> 203
 <211> 895
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(895)
 <223> n is a, g, c or t

<400> 203
 ttttttcgng gattnctnnt ntntnnntnn ntcccccat tnnncttggg gggnaannnc 60
 nacgattcan gtnttatnnc tacgaacaac cattgtgagt agaaccatct ggatttttnc 120
 tcactttcat ttaaaagact ctgttgatat tctaggtact gattccatat atcagtatca 180
 acaaatttct caaccaaggg gataattggt ttatctgttt gcaattcatt ccgtaattta 240
 gaaaggagan anntttcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa 300
 atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcn tgtctatgca attcctctag 360
 ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc 420
 tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata 480
 tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt 540
 actacagagg gaaaggaacc cctgacagat tttccatgtn ttttcatgct tccatacaca 600
 ttnttctttc accattgaca ccnactanaa aaagaadaccn gtggnccttt ctgagggttt 660
 ttttttngnn anntnaattn ntntttttta aacttggntt ttccncctna attnttancn 720
 taggntnana aaangaaana ntgcctnnna tnaaaanggn ncctncaatn ntatnttacn 780
 cnnanaagnc cnattggnaa gggngcanaa antntnanng ggnnacnaaa ataaaannaa 840
 aaataactct nnnanccttt ggttttacat taacnaaana nntctncccc caana 895

<210> 204
 <211> 887
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(887)
 <223> n is a, g, c or t

<400> 204
 ttttcnngng gntnnnnnnn nnnnnnnnnn nnaccccnng tnnnnntngg ggggaannnc 60
 cnncccacga gnattttttn ctcaaaaaaa aaaaaaaagc caaagtcctc aaaatggcct 120

```

gcatgggaact acattctctg gccctttatc agcactctga cagctctctc ctttgcttat 180
tttgctctctc attctagcct ctggatcttt gcccttgctg ttccttacgc tcttctccca 240
gggatctgaa aggnttacac cctcacctcc ttcagagggt tgctaaaatg tcttctaccc 300
agngaagcct tccccaacca ccacattaaa aacacacaac cagcaccctg tctctatctt 360
ccttcacttt gcattngncc attgngtaac atcacttaca taccttnaat tnttagttna 420
ttaattcata ctgcaaaaaca acttantttt taccatgtgc caggcattgn ccctagttgc 480
tgacaatata gnngaaaata aaatagacaa aaatcccatc tttngaattc ttngaacctt 540
acattgggag tgacaggcaa aaacgaggna aatcagnaaa atacgtgaga cagaacgcta 600
aaagaaaaaa aagaggaaaag ggctganntt ngngncttcc ctccanaatg caagctcctn 660
gagaatacag annngngngn nnnnnacnac ngnatctccn gacaatagcn cccannacan 720
annangcatt ncnaccsaan tnnaaaaang annaacnang gcannnnccn aannncnggc 780
cacatnncaa ccntaaaaca anaanacca anaaaaaac ngnnncagcn aggnacacnaa 840
nnaagaaana nccgnnncna attnnnggng caggccntna aanncca 887

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<210> 205
<211> 843
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(843)
<223> n is a, g, c or t

```

```

<400> 205
acccccccca tnnnnttggg ggggaaaaac canccagtaa nagttttggn gcaaggngng 60
tggtctttaa tcatcagggg caaggtagat ttaattctcc attatccatt aattatttaa 120
tgaacaccaa cagtgggatt gcaagtggga ggtttagaac aacaggggtc tgtggcaaag 180
actactagac catggtatca ctagggacag ctagttgggg aggcnttnng ggtattactt 240
ggcttataaa accaaaatag accaacagca gattattaaa atgctggtgt tggctgccaa 300
gtggaacgta ataatcacac atctggtttt ccaaattgaa cagttcttag atccagaatc 360
ctgtgattga tagagatgct agatcctttt gcagaaaatc ttataatgcc ccaatgaatt 420
tatagtagta atttcccaa tcttctcca aaagaatcta tgctgcagaa aataaaatac 480
ctgnacagng ngcattacat tngcactac agagatgaaa gtagccaaat atttcaagt 540
ctgnngaate canagttnga gatgacacca ataccagaga aaacaaaaac catcatgatg 600
ccctggntag gnggggtgtg ngaaanccan gnggaaaaan aaagncttgg gcccnacant 660

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ncanatataa atgnncaaag agncnggcna cccnccccgn naanaaggnn agggncnctg 720
 nnggccnaaa nnaggnnngg aagcaccnaa anaannngaa anaaccccc accaaaaccc 780
 ccngncnccn gaccnggana ggggggnncc cntncncann ccaaaanggc ccannngnnn 840
 ncc 843

<210> 206
 <211> 927
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(927)
 <223> n is a, g, c or t

<400> 206
 ncncnccccng gnaanccccn gngtaannn nnncccccc ccaatanntt tgggggggna 60
 annnccccnn canagtgnaa tantaagnaa ncaaaggcag cngagtcagn accaaaacta 120
 acagnanaat aacagnaaaa nnnccaccac catatgaaag caggggaaaa atatatggaa 180
 acagatatgg ccaaaaaaaaa ggatgcagac aacgaagnaa gcggacagaa gcccgagaag 240
 aaaaacgggg ncggggggaga aaggagacta tnaataggaa aaangaaaa gcanacacag 300
 ggcgactgag caatacagaa agcaaagang cnggataaaa agcagggccc tagagtggga 360
 gtggcncaac acgaagaggg gcacccagag ggggaacaca gcgcngggng acaggagggg 420
 gnccaaaang gaggaaaagc gcccnncna gagaaccanc aggcgcggcc cccccgggg 480
 cggcagccgg ggagggggcc cacagangng gnggagaagc caagaaacnc agcgganggn 540
 agggaancac nggcccangc gcaggggaca cccccagaa gccnaggaca gagggagggg 600
 caaggngcac actaagganc cnnnaangaa cggccagagg ngcaggancc cacannagaa 660
 gnacccngaa ggggcaggng caggcaagnc cccgcngcan gaggacaaaa cnggccngcn 720
 gaaaanggnc gccccnncac cccnccngnc cnaaaccac ngcaaccacc agncnnnnac 780
 annaancn aaaacacaaa ngccccacn nnanccancc cganaaaagg cnaanaacca 840
 gngnnaancc naccacccng gncnnganga cccnggaaac cnnnanncca nncnnaannn 900
 nnacccnaaa ccaaaagnnc gannacc 927

<210> 207
 <211> 940
 <212> DNA
 <213> Cercopithecus aethiops

<220>

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<221> misc_feature

<222> (1)..(940)

<223> n is a, g, c or t

<400> 207

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ccccggnatc ntttctgtnt nntnctnnnc cccccctta ttttgggggg ggaannnccn      60
nnnctntnnnn nnnttttcca ccnaaaacta tttnttntnc tnncccgccct atcctccaaa      120
ctagcaatan ttcggttctt ccctcttgct ctcgggcgga ttcctgaaag tcgtttattc      180
tettaattaa tacgccgctc cagccccgcc cgttcagctc attctcttaa tcgcattacc      240
ctggctgcng nnnctttttt tttttccac ctgctgccac ccaccagac accgcctncc      300
gctctttccg gaccatctca gtttctctc ctccccnngn cccaattttc tttaggctat      360
ttctggctcc cgtaggtttn tcatgctctc gttagcccca ccccatcacc accancggct      420
ctttttcggc tctctccnng cncctcctgt ctctgctca ggctcttttc cagctattnn      480
cgactccctt cntactcacc ctttgcttc ngaaactntc ccaccngccc ttcaggcaaa      540
tcngtctcna cccctantc ccgcacgtga acacagncct nccccctccg ccttcttaga      600
nccccctct caccnnnncc ctttcnnc catcctcaaa actananggn tgggtacngg      660
ccnancncc cnttttggtg nnnnaannccn gaatcgccn caaggncctg gtncntnccc      720
ngaaaancct atngcnngn cacaacang ggaacannn ttcncaccn ttntccactg      780
anccncttc cccntcacc ttnaaanaca ttntttnnnt ttatctaaaa ccnttcanc      840
ccnctctct tcgncacct cnttntant ncccatatan cccntagnt natnctnca      900
atncngcac cnnntntnta tctaataaaa cccaacccc      940
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<210> 208

<211> 881

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(881)

<223> n is a, g, c or t

<400> 208

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ttttccnng gnnattcnnt gttnaatntn ntntcccccc cattntttgg gggggaanac      60
ccgnanttga aatttnggga caaacaaca tanccttttc tctttccttg aagggttaat      120
gctccaacca gcctcagatt ggttcgctg aatcttaaaa ttacttttct ggtcacgcgc      180
gccgaagggtc taagcatttg tgaaatgtct tttttcccc ccccccccc ttgatgctgt      240
tctctttggg nttttttaat tacacagggg ttgagaaacc aaattaaaa taggcgtgtc      300
tggtcaacag tgatcacgtt gcatgctttt agctttgntt gttgaagttg cttctctcc      360
```

```

ctgagtgget ttcttccttt tttttttttt ttttttattt taaaaaggaa atatcataag 420
ctctttcaga aatactcaca ggaagtgagt gtccgtatgc tggttactca ccancaactg 480
agtgttggca ggtggagaat gctaccgcag ccgcccagac agatctgcag actggcccca 540
ttgcagagga ttagacacag ggtgcgtgga tcatagggtt tttgtacaga angcagtttt 600
aagaggaaat tggtcactgc atgtcatctc gaggggtggt gattcangga gccaggcctn 660
gggggttcana aagnacgttg ctngccatct tnggaggttt cctgctcact tntcaaangg 720
ncaggctngc cttttaaaaa tcaatgttcc ttccaccccc aaaagggnntt ctttttgcag 780
tgaatcanct nccaaaataa atagcccccn tttttttgga aaagaacgtt tgnaaatccc 840
ncnttttaat ggnangtttt naattngggg gttnantcaa a 881

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<210> 209
<211> 896
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(896)
<223> n is a, g, c or t

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```

<400> 209
tttttcnngg atnttnattt ntnacttat cccnccatt attttanggg gnaancctt 60
nncanaatat tgtnttacia atatcatttt nggtgatgta tgtcaaaacc aaaactgcct 120
ttatgtcaat atgctgtaaa aatctatcag aatatactt aattcttaac tttcattgtt 180
gtctgtgggt tgtcttgtat aattattatc acatctacag tattttctgt aggtaaatat 240
gaaatgtttt tttnatgtac cagggggaaa atgcccttta ataagccttt ccctagacaa 300
agcaccattt aggcgttttag aagcaagaac tagtganntc agaaattgct gtcatacata 360
ctcacctgtg aatgggtcgta caaaggatcc caagcgcagg acttgcctg gaagcagagg 420
atcggtattc accaggaaaa gaggaagta gaaatgcaa atgccagcgc tccctttccc 480
cagctcatct tattttagg cactcagatt tttggaatcc tccaggacta acaaatanaa 540
accacactag gttgtttttc ctaattncct gtgaaatgag tcangtangt caaacanctt 600
atccactcca gagagagaac caattccttt gagctacact ccctgttttc cagtnaccct 660
aatnccctct ntgggtgtcc ttgaanaaag ggnntgccna ccantgcatt ggagagccca 720
ccgggtttnt gaatgaagan nattgtnaaa antnnccaaa aagttaannn gccttcaagg 780
gganagtttn cctttntgaa nattnaagna ggaaaaatcc cannttaaaa tacctgggnt 840
cngtttttt nntaaaaaan cnnnnnactt ttttttggnc naangntttt tttttt 896

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<210> 210
 <211> 869
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(869)
 <223> n is a, g, c or t

<400> 210
 nnccttctaa tttnttagtt tnnnagctca cttataaanc aggctacagt gttattctta 60
 agtattcatt gttgtataac aactacccc caaaatttag gagcttaaaa taacagcaaa 120
 cacttattat ctctcatggt tctgtgtggt gactagacat ttcggctcct gtgcagatgg 180
 ctggagcact gagctntttt ttnggtctac agtgctctcg cttacatagt aggcactagt 240
 gttggctgct ggtagcaagc tcagttgggt gtgttgacca gannnnttgg ttctgctcta 300
 gagcattgta atantgagca tttcaacagt attaacccaa catgcaaaca ctactatag 420
 taagcaaaat aaaataaaat aaagccccc cccagatata tatgctctaa aacttccaaa 480
 cgtatgaata tgtnacctta aatagcaaaa ggcactntgc agtgtgattn angcaagatg 540
 gggcagagtg tctgggaata tccangtgga acccaataat gcaaataaaa aaaatcnttt 600
 tataanangg naggtaggaa ntaanacatc tgntcancat taccgctgcc nggtttttng 660
 aaaaanaaaa ttnggaagaa agggggcnca agccaaggga atnccaggga tttcnctaan 720
 tnggccaaaa caanannatn aaaantcntc ccccnnnnc cnnananaaa aaantgnaac 780
 cctgggcgnc cncnttgatt tttnnnccca angancctnc ctnaccaana nantnaaaaa 840
 aaaatctntt gntcgnnttt nancnaaan 869

<210> 211
 <211> 874
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(874)
 <223> n is a, g, c or t

<400> 211
 tttttngggg atttcccttn tanantnnan cccccccctt anttgggggg gaaatacnnc 60
 ccattaacag ttttaactgc agcctctgct tngtctacat ctgctgcaa cttttaacta 120
 atggcgagat actttcgcta tttccgatgc cattaggaaa caaatagaaa aatagtttgg 180


```

caacaacatc ttctcgaata ttatcacttg acaaatttta acgttttagg tggaaacgga      240
attttaannt tttgttttaa gaagcttaaa aaaaacaggc atgcttaatt agcataatgc      300
tgaatggcag ccaatcacia actgaatfff taaagcnnga agtgtttgct cctggcgtgg      360
cgcgccccgc tgtaatccgg gaatcccagc gttttgcgag cccacgcca ggccgaggag      420
ggaggatcct ttgttccacg agttcgacac cagcctaggc aatatagcag aattcagttc      480
aatgactcta ggcttttagcc atgcagtatt aacaaatggg atattaacaa tattaacaaa      540
tgggataaaa accaagaact tgacaaatgt gttaatttcc tatttctgtt ttaatacatt      600
acacaaaact aactgcctga aaacaaaaca aaagntntta tttttatagt tctctaaatc      660
agaanttttc attggggcnc aaaatcaagg tnntctgcaa ggctgcattc tttntgnagg      720
ctgtagggga naaatttcat tgtccttgnt ngncctttaa naaagcctgt tttnccttgg      780
cttggnngcc cctttttcaa ttcattttta aaaccccnan nnnatnngnn ccnntttctn      840
cctccnctc cncnttaaaa natTTTTnt gngn                                     874

```

```

<210> 212
<211> 866
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c or t

```

```

<400> 212
annnnnnnnn nnnnnnnncc ccngatann ttggggggga aannncnca tttgagtgt      60
ncaggggcaaa accaacagta aaccagacta ctaaagattt acttgtggaa tttttttgca      120
aagtgtcaaa gggcttatag agaaaatgaa acagttcttt aaagatgttc ttgagcgagg      180
tttttttttt tttaacttac taaaagactt tatgttttag aacagttttt gtttacgttn      240
agcacgtagg acgtccccac tacacacaca gnttctctta ttaatagata ttagtatggg      300
acattngntg caactaatga accagtaatg ataaattatt aactaagatc catagnnat      360
tcctgcttcc tcacattnta tctaaagncc tttntctgnt ccaggatccc agctaggaga      420
tngaaagacc ccacctgnag gtnnggcaag ctagctgagg atcgnnncgc atgatngaac      480
aagatggatn gcacgctggn tctccggccg ctngggngga gaggctatnc ggctatgact      540
gggcacaaca gacaancggc tgctctgatg ccgccngnn ccggctgnca gcgcaggggc      600
gcccggnncn tttnggnaan accgaccnng ccggngcccn gaangaacng caggacnagg      660
canngcggnn atcgnggntg gccacgacgg gegnnccnng cgcannnggg cncnaegnng      720

```

nnacngaaac gggaagggn cggcngnna nngggncaaa angccggggc aggaaccncn 780
 gnnnaannaaa ccnggnnccn gccnnnaang aaccanaang ggngnnnnaa agnggggggn 840
 ngnananccc ngnaaccggn ncccc 866

<210> 213
 <211> 998
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(998)
 <223> n is a, g, c or t

<400> 213
 ttcgggggtc tanaangtnt nntnntncan ncccccccn tttttggggg gnaannncnn 60
 nccagtttnn natttggnnn nggagcataa attnagtcgn ctctctcacc taaaactcat 120
 ggtctggtgg aggctccgcc tcctttgtcc cctttcatgt ttctgtctca gcatgcctgg 180
 ctcccttaagg ntcttcatct ttgtcaggtt tatctcaagn ctcaattgaa ccgccncctc 240
 ctgncaggcn tttttnnnct gggaggtgag cagnngggtc cgggaatgtg ggagctaagg 300
 gcatagatgt gaggaccncc ctatgaanag gaaaaggann cnnctggaat gcanacctgg 360
 gactgtctgt atacctgcct ggtcactaaa tttctctgag aggcataaac agnnaaaanc 420
 ctganagggt tatngccaag agcatngatg gggctctgctt tctggganc aggaataaaa 480
 ggnngtgata cccanagga ttatntctca gccaggncctc tccttccnt gtangannag 540
 tcccttgagc cncnnncna ctanancntn ttttnaatna aacnccctn tnnncgggac 600
 aacgggaann tccctatann cctcccannc tnggttgnnn aanncccggn gctaaaagca 660
 atcnnncntn nccntnggtc tncacaaaan ggctnagaat naccangttg nagccccntn 720
 ntncctant cccccctgna nnnctatnat ttnttccaan taaccaatna nccccccan 780
 aaccannat acanacaaac atngaccccc ntcaaaacca acanccnnnt agacntntn 840
 ccnactnnt agnecatng cnaaccgnaa gcntttgttn tngaanttan ccaagggcct 900
 cncnaacaan ttcaaaaana agtggtgntt ccccccncct naaccccgng cccccacnt 960
 caacanant aaaaannaan acccacncc nntngtng 998

<210> 214
 <211> 956
 <212> DNA
 <213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(956)

<223> n is a, g, c or t

<400> 214

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ttttttcggg ggattnctnn tttnttnnt tnncccccc ngtnnttgg gggggaannc      60
cancgttctn nctatttctt tcttgacgag ttnttctgag cgggactctg ggggtcnaaa      120
tgagctagcc ctttaagtaac gccatthtgc aaggcatgga aaaatacata actgagaata      180
gaaaagttca gatcgagggtc aggaacagat ggaacagggt cgaccggtcg accggtcgac      240
cctagagaac nmtttntgt ttccagggtg cccaaggac ctgaaatgac cctgtgcctt      300
atttgaacta accaatcagt tcgcttctcg cttctgttct ntcgcttctg ctccccgagc      360
tcaataaaaag agcccacaac cctcactcg gggcgccagt cctccgattg actgagtcgc      420
ccgggtaccc gtgtatccaa taaacctct tgcagttgca tccgacttgt ggtctcgctg      480
ttccttggga ggggtctctc tgagtgattg actaccgctc agcgggggtc tttcaatctg      540
attgcctctt gcttgacggc aaggagtccc gaccactgaa cactgatgac ctcatctggt      600
gtgattgtct cttgcttgac ggcgaggagc cccgacgact gaacatggat agtcgccgcc      660
acagcacggt gatcanaagg ctttcgttcg acttatgant ccgacgntcc ggggagttca      720

aagccccctt tcnactcent gggncctttt ngtnnttntc ttgnccacct ttcttgactt      840
cttnaanttt gcttctggan tgntaatnnc natcnnaaan ccttgtttgn aaaancntgg      900
ccccngncc cngnttctt nccccccann tantgnttta ngncctntt tggaaa          956
```

<210> 215

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(915)

<223> n is a, g, c or t

<400> 215

```
ccncaacctt ngagacccta aagacattgg agcagcccca tacacctcct cccagggcac      60
acaaaggccc ctgacatgcc catggcagtc caaggcctcc aattggagcc atctttggta      120
aatctggggc ccatcagccc cactgcctt tcttggtagc ctgagcatgc tggcaagggg      180
actnnttttt gcattccatc ttgtntcata taccacagn acctgatgtg gacatgactc      240
accctggggg cctgtgagtc aataagggtg tntgantaag gggcagagca tttcaactta      300
gtcccataac ccatgagctc attaagcaaa tattacccat gcctagattt ggggccagtc      360
```

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| actaccact | ggaggctgtg | ggctccaagg | tatggcagca | ggggaggcca | gccaggcntc | 420 |
| tgcccagctc | acccttcctt | gtgaggatgg | acnccagcca | ggcctccac | ctccaccct | 480 |
| agactggggg | accggtgtt | ggggggcaag | aaaggggacc | tgaaagtggg | tgtctnggag | 540 |
| ntaagcccat | ttctttnata | ctccnccaat | aggganccaa | gaagnggggt | tnagagttac | 600 |
| cccaanaact | caccccaacc | cantntnaac | gctgtggggg | ctcaangggg | acangcnaaa | 660 |
| acnaaaantn | anacngggcc | aaaaaagaac | aggtncggnc | ctncccnan | ggaccttttn | 720 |
| ttttctacca | ccttacccan | nanaatnctt | gaccaggggc | ntttcccaa | acncngnaaa | 780 |
| anctttcaag | cntngnact | ntnnaaccc | ngggcnnnnn | aaggnntagn | gcctctnnn | 840 |
| ancnctntgn | cnggttncca | tngnntaaaa | acccaangn | aactcctcca | aanaacaagn | 900 |
| anccnntctn | ggttn | | | | | 915 |

<210> 216
 <211> 949
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(949)
 <223> n is a, g, c or t

| | |
|------------|---|
| <400> 216 | |
| tttncngngg | nanntttntg nggaannctt nncnccccg gnttttttgg ggggnaannc 60 |
| ncatcgttct | tactattgcc ttcttgacga gttnttctga gcgggactct ggggttcgaa 120 |
| atgagctagc | ccttaagtaa cgccattttg caaggcatgg aaaaatacat aactgagaat 180 |
| agaaaagttc | agatcgagggt caggaacaga tggnacaggg tcgaccgggc gaccggtcga 240 |
| ccctagagaa | cctttntatg tttccagggt gccccaagga cctgaaatga ccctgtgcct 300 |
| tatttgaact | aaccaatcnn ttcgcttctc gcttctgttc ncgcgcttct gctccccgag 360 |
| ctcaataaaa | gagcccacaa cccctcactc ggggcgccag tcctccgatt gactgagtcg 420 |
| cccggttacc | cgtgtatcca ataaaccctc ttgcagttgc atccgacttg tggctctcgt 480 |
| gttccttggg | agggtctcct ctgagtgatt gactaccga gtggggaacg ggggcagggc 540 |
| gggtgggagg | agggcgaggg aggctgagac agcccagggt agagagggcc aagcttgaaa 600 |
| ggttttccca | ggcttgggga gaggccttg tcaggatgtg tatgggtaag gggtgagaga 660 |
| cagaggtncn | tggggcangc ccggacctgt tttttngnc cagtntcagt tctgnttcnc 720 |
| ttgnccctga | gacccacgt tcanagaggg ttggnnccgt tnggggnga cnnttanccc 780 |
| catctgatcc | catggtggnn ntganganan gggctaannc nnancccntn cagtccttn 840 |

ttgcccncac ccgggccccn atcnngnga agagggagnc cgctcgncnc nccccagga 900
agggnnncngg nanaccggnn gnccccngng caaccngnaa ccaacnnan 949

<210> 217
<211> 999
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(999)
<223> n is a, g, c or t

<400> 217
ttttcccngg gannnnntg nnnnttnnnn nttnccccc cccatnnnnc attggggggg 60
aaatncccc catntaggcc tttngcnaa agaccagtn ntctgccctt gggtncncnc 120
agganctctg caatggggaa gtgagccctc ctgaggcctg gctggcagga ggctcttcaa 180
ggtcattgtg acttccccca acacctcgag tttctgcaca gcagccacgg agacgggcct 240
gggggctggc gggaaatttt tnnnaaggca atgtttncct gagtgggctg aaacctgaga 300
tgaggaaatg agaagacgtc aggtggctgg aggacacggg ctttaggaca gccagcaccc 360
agccctgtag ctgaggcctc cggagggagc cagagggaaa gggagtcccc tccccgggc 420
ctgagtctct gccagtgcc agcactccca aaggatccac cccaacctga gagaccctaa 480
agacattgga gcagccccag acacctcctc ccagggccac aaaggcccct gacatgccca 540
tggcagtcca aggcctncaa ttggagccat cttttggtaa atctggggcc catcagcccc 600
cactgncctt tcctgggtacc ctgagcatgc tggcaagggg actggaaact gcatcccatc 660
ttgtctcana taccacagn acctgatgtg ggacatgact caccctgggg tcctgtgagt 720
caataagggg gtttgantaa ngggcagaac nnttnaactt antnccanaa acctatgagc 780
tcattaannc aaanttacc tgccatanaa nggggccant nactaccnac tggaaggttg 840
tggcttcang natggntnag ggaagncnc nggctttccc aannnnncct tnccttngag 900
ngggaccac cagcctccan cnccccnaa actgggaacc nngngnggca anaagggcng 960
aaanggtttt gantaaccna tttntanncc cnnggnaaa 999

<210> 218
<211> 962
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(962)

<223> n is a, g, c or t

<400> 218

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nnnccccggn actttcnntt anngnanncc ccccccctnat ttgggggggna annacacann 60
ttannnatttt nnnnnngaca aagctttttt ccagggnntg aacngcngga tatttcctnn 120
ancaccatag ccgncatagg gcttccaaat atccctttgc catttccaca agaactgcct 180
tatcgaaagg cttcttgaag ggaaagatgt aactctgnga gatgaatnct ccagaggaaat 240
cctggatnnt ncccataggn angnctnaac ctgttctctc cngancttng ggagggtgca 300
cctggaagca agctctgggg tccctgggag agaaagcaca gcccctgccc tggagacact 360
caaagcctgg aagggaaggg cagngggctg gacagagacc acaggtgtga cggtcctagg 420
tgggaggtgg gagctcagag ggggcaccta accccattgg gcagagtgtc canggaaggc 480
tttgagtagc gccncagagg atgcngnaga ananccccag gaggagagcg acngnatgna 540
gagggaanag catttaccgn ngcctgggag tngagagagg ctggcnggag aaaaagagc 600
tccangaagc cacaaancct cannagnngc gtccacagcn cgatnctcna ncaccnacia 660
cananccccg ccncatanaa agngcnccaa nccatcnntc acngaangaa nnaacaaaat 720
gaaanaaggg agatcaccna agggaganac gcngacaccc ccccnccccn accnganaac 780
cacnncanaa cntnnacccc gcanaccnaa ganccatgaa ganttnagca cggnanggcc 840
cannnaaaag ncataaanan aacngnagga aaagggaccg gacacccnan tnactacccc 900
cacnntacc caaaaccaca ncnnngccn gggcgnaacn cccnacnacc aaccancccc 960

```

<210> 219

<211> 891

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(891)

<223> n is a, g, c or t

<400> 219

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tttttngggg nttnnnnggg gnnngnnnt cccgcctnnc cttngggggg annccctnnc 60
agttgggaat tnatttaaag aagggaactta agggagatta ttaaagagcc agnaacgcaa 120
aggagagctg cggaatcga caactaccga agacggaag cacattcacg aagcggtccc 180
ttcaatccgc aactacact cccacgaccc gccccttccg cccacagagc ccgccacttc 240
cgcctcanan ntnacgccc ctctgtgtc ctaagggcct tcccgggct gatcagagcg 300
cccgcccctt agccgcaaca gaagccgtaa agctttctcc cgtcgcatg cagcgctcaa 360

```

```

ggcgccctgcg cagaccctga aaagcggcca ggggtggcccc gagcttcctt tttccggttg 420
cagcgccgcg cggttaggtt ctctcgttct cgctcgcagc catgccgtcc aagggccccgc 480
tgcagtcggg gcaggtcttc ggacgcaagg tgagctagac gccagatggg aaggggaggg 540
gaaggagaag gtcaggggtct gggagaggac ggtgggcagg aatacagggg gcaacatggg 600
agctggatcc cgagctcacg gggccacact ctcttgatc ccacagaaga cagccacagc 660
tgtggcgcac tgcaaacgcg gcaatggtct catcaagggt aacgggcggc ccctggagat 720
gattgagccn cgcacgctnc aatacaaggt gnttggcatt gggncattcg ncgttgantt 780
ggattggagg acctntngga nataatagta gctnnttgaa agcttgaggg ggcnggntnt 840
cancanccgg gnttttnana anttngnttn gtntnnnnaa aaggggggtt t 891

```

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<210> 220
<211> 902
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(902)
<223> n is a, g, c or t

```

```

<400> 220
ttttttnnng nntataattt ganntatnta tccncccat aaaccttggg ggggaanaca 60
aggncnaag ttttttagga ttgtgctact gtactccagg gtgagtga gcaagtatac 120
tgttcttaaa aaaagaacct tatatattaa aaaaaattt ttttttaact gacctgcaa 180
tgcacatatg cttcctttta aaagtagtaa acttcagaag gggcagaaat cagactctgg 240
tttctttcca ttttnagcca aagaaactga nagtnccaaa cagggaacag aagaaccct 300
ttcacaagca agcatttaaa cagaccctaa ttcggccgcg cggctcacca ggctggtcag 360
gagttctaga ccagcctggc cgacatggtg aaaccacgtc tctcctgaaa atacaaacat 420
tagccggccg tgggtggtgt cgcttatagt ccagccacc cgggaggctg aggcaagaga 480
attgcttgaa cccggagggt ggaggttgca gcatccgag atcgtgccac tgcaactctc 540
agcctgggcy acagagcgag actccctctc aaacaaataa atngaaaaaa aaataaacag 600
acccaaattc aagctatttc aatacttact gagcacttac aatgtctaaa acgctgcttt 660
tagacgcctt ggggtttnt taaggatnaa aacacttgnt nctngtgaa aatnaaanct 720
atgaaaactg ggtgttcctt caanccttn gggntcccc ccgnttccc cnntnaaat 780
gaaccttnt aaacattnc aattttnaaa agncancccc nttaattnt taanacccc 840
ccaatttnaa nnttttaaan ttttntnaa acnntaaanc cccgggtttt ttttnncnaa 900

```

aa

902

<210> 221
<211> 907
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(907)
<223> n is a, g, c or t

<400> 221
ccncannggt agntccgctc gccttccgcc ttgtaagcng gaaaggtgct tcgcgaggtc 60
tcgccttcgg ggtccgacat ggtgaccgga tttagagacg ctaaagcaga gacaatcgaa 120
gaaaagctgg agaacctcta tctggttctg gtttgtggaa gctccgtctc ttagcaaccg 180
cgagacgann ttttcagcga tttccgggtc cgtccctgtc tggcaagggc ccggattctg 240
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gagtgcgtgg ctggcggctg agctccttag tgtttctgtg tgcacgctcc ttcggttctc 360
tctggagtta ctgcgtgaaa aggctgcctt gtaagacagc caagaaaaca ggaagagggt 420
tggaggcaaa gtccnaata gggattgaaa gacccacact gtnggttttg gcaagctagc 480
tgaggatcgt tcgcatgatt gaacaagatg gattgcacgc tggtttcttc ggccgcttgg 540
gtggagagggc tatttcgggt atgactgggc acacagacat tcggctnctt ttantgccnc 600
cngngtncng gctgtnagcg naggggacgn cccgggttct ttnttgnaaa gaccnaccg 660
ttccggtgcc cttaatnaan ctgnanggac gagnnnancc cngntttatt ttgntgggcn 720
ncaacggncn ttccttnnac anctngntcn ncancnttgt nanttaaccn gnaanggnnc 780
tngntngttt tggncnaaat annccgggca aggaactccn nnnnannccc ccgtgtnnnt 840
nccccaaan tatcnattng ggtancnaan cngggnnnnn tnaccnnnac ccgnnnnccg 900
ccnanct 907

<210> 222
<211> 955
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(955)
<223> n is a, g, c or t

<400> 222
tttttcggg ggaannnnnn nngggnnnnaa nnnntcccc nccccatnnn ccttnggggg 60

gnaanacccc nnncaattcc ctatttggn aactttgcctc caaccctctt cctgttttct 120
 tggctgtctt acaaggcagc cttttcacgc agtaactcca gagagaaccg aaggagcgtg 180
 caacagcaaa cactaaggag ctacgccgcc agccacgcac tcactactct cgggcccggt 240
 gcgcggcaga actggcgcac nnttnnnccg gcaggttgca cccagaatcc gggcccttgc 300
 cagacagga cggaaccgga aatcgctgta cgtctcgtct cacggttgct aagagacgga 360
 gcttccacaa accagaacca gatagagggt ctccagcttt tcttcgattg tctctgcttt 420
 agcgtctcta aatccggtca ccatgtcgga cccgaaggc gagacctcg gaagcacctt 480
 tccctcttac atggcggaag gcgagcggt ctacctgtgc ggagaattct gtgtgaaatt 540
 gttatccgct cacaattccc acacaacatg agcgtcagac cccgaagaaa agatcaaagg 600
 atcttctttg agatcccttt ttttctgcgc gtaatctgct gcttgcaaac aaaaaacca 660
 ccgntaccag cggnggtttt gnttngccgg atcaagagnt accaaantnt tttttcnnaa 720
 gnaacttggc ttnagcnaa cccnaanacc aaatactgnc ntttngngta cccgtantta 780
 ggccccccct taaaaanttn nnanccncta atancngtt ttntaatttn ttacaanggg 840
 tnttgcnagg gnaaaaattn gttttaccgg ttgnctnaaa aaaattttcc gaaaggcccn 900
 ngtnngntaa aggggntctg cccaacccat tgggnnannt cncccannt naatc 955

<210> 223
 <211> 927
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(927)
 <223> n is a, g, c or t

<400> 223
 nnnntttta aanacnnanc cccccanta ntttgggggg gaaaaccccc agcatgccca 60
 cntatcatnn cccatcactg ggtaatatc acagnatcaa attatcctcc ctaaccagtt 120
 cctgtgaata ttctcattga tctcaaaact cactttggcc tcagtgatcc ccaacagcct 180
 cctttacaac cttaacaat ccaagttcct gttctgtgag agtttcctct cgaaacacaa 240
 cattccgtac aattcagtct ctactccgt caatcctcta cattggcagt gagaccttat 300
 tttgtgacct ttactttac agcagccatt tcaaagagac attctctagc ctgaaagggc 360
 tccagattct tcaactttc tattatgtat gcattgcaa tattgaattt gcactatctt 420
 atcaactatt ctaaaactac tgacatttgc agaaactggc catttggtct tagggaaaat 480
 gtctgtgtta tccaaaaatg gagattaaaa acttgcacac attcctactt gatttcaca 540

gngacctgat ctatggtatc tagcntcctt cccctctgcc ccaagttcac atttccatca 600
 gctcatatat actcttcctt ttctactcct gctgacaggg tccaaggata ctgcctcaaa 660
 aactctataa aaganaataa aaactnatta actggctttt ctatcnaaaa nctttcnact 720
 agnaatatta anaaangntt ttcaaccggt nggatccgaa ancatccnaa gnagggnatna 780
 ngccnaaaaa aaaaataatn nntttcccn aaaaannaaa aaatagnntn tnangggggc 840
 ccngnncntn gnaaaagaaa naannccggn cntnnaaana nnannaaaaa nntccncngg 900
 ntnannnnn aaaaancatn aancnnn 927

<210> 224
 <211> 936
 <212> DNA
 <213> Cercopithecus aethiops

<220>
 <221> misc_feature
 <222> (1)..(936)
 <223> n is a, g, c or t

<400> 224
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 cctagaagca aagccacagg aataagtcag ctttcccaga ggtcaaagaa ggctgtaggg 180
 ccacctgcca cgcctcccgga ccccgccgc gcggcctggg cccgctcccc aaccaaagag 240
 gcccgaaatc agagannttt tagcagtttc acagaaagct tctttccagt tttgaacgga 300
 agatatttcc tttttcaccg taggcctcta tgggcttcca aatatccctt tgccaattcc 360
 acaagaacag ccttagcgaa aggcttcttg aagggaagaa tgtaactctg tgaaatgaat 420
 tctgcttata ggtcttgaga taaagtcacc gatctcatat catggattat aagggtttcc 480
 ttctattttc tggcattttg gatattgtaat gatgagcatc agaaagttaa atcatattta 540
 atttttagaa ttattaaata ctctgaggt cattttgggt gattttgngt ggctttcaac 600
 cataaagaga tcaatgcctt gcagatataa agctttcctt ttccttcttt aataattnta 660
 aactctgaat tnatgnctac agatatntaa tngatcataa atganaaatg ngatactatt 720
 cnetacctcc ttatctgttc tcggaanaga ctatacancc ctgcaannat ngaagttnan 780
 gattgcttnt acgaaannna aaaaaaatn acttnttttt nggcaanana aaatgcttcc 840
 tccgttgnaa actccctca nggngtntta ggggnannn taccttnaan ttcctngnc 900
 ctggnnnng tnnnaggan tgcaaanngn tttctt 936

<210> 225
<211> 605
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
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<223> n is a, g, c or t

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ttaagaagat agtccaagtt aaaggcatac attcaagcta gtggcacatt cggaagagca 180
gacaaagata gttgggttga aatgggaaat ttaagccatg atcttaaaag gacagaatgg 240
atatttgtta ctttttctat gggaataaatt gatttttttc accttcctt tcttggtatt 300
tttttttttt ttaaattagt ttgggtactt taaccttact gtcggttata ttggttctct 360
ttttatgtct gagttttttt ttttttttga gacggagtct tgctctgtcg cccaggctgg 420
agtgcagtgg ccggatctca gctcactgca agctctgcct cccgggttta caccattctc 480
ctgcctcagc ctncctagta gctaggacta caggcgcccg ccacctngcc cggctagttt 540
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ntcct 605

<210> 226
<211> 654
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(654)
<223> n is a, g, c or t

<400> 226
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antactgttt gaggaagac tgaggntcag atggcagagg ctccntagag gaaggaggct 120
acagccttga gggcatcagc ttccacact cccaacctgc tgcctctctc tgctggaatg 180
aggagggggc tcctggctgg gggctctccag ggtggaggga ggagctcaca ttcttagcat 240
tcctnttnc ctagtttga aggaagacct ggtgagcatg ctgacccag aggagtgact 300
caggcccatg gctcgagtgc ctgaggagg accagggtcg gggatggggc atgagtcagc 360
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PCT/US2003/037143

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<210> 227
<211> 2635
<212> DNA
<213> homo sapiens
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<220>
<221> CDS
<222> (285) .. (1679)
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151

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| Val | Leu | Lys | Ala | Leu | Ser | Glu | Glu | Lys | Asp | Val | Leu | Lys | Gln | Gln | Leu | |
| | | | 120 | | | | | 125 | | | | | 130 | | | |
| tct | gct | gca | acc | tca | cga | att | gct | gaa | ctt | gaa | agc | aaa | acc | aat | aca | 728 |
| Ser | Ala | Ala | Thr | Ser | Arg | Ile | Ala | Glu | Leu | Glu | Ser | Lys | Thr | Asn | Thr | |
| | | 135 | | | | | 140 | | | | | 145 | | | | |
| ctc | cgt | tta | tca | cag | act | gtg | gct | cca | aac | tgc | ttc | aac | tca | tca | ata | 776 |
| Leu | Arg | Leu | Ser | Gln | Thr | Val | Ala | Pro | Asn | Cys | Phe | Asn | Ser | Ser | Ile | |
| | 150 | | | | | 155 | | | | | 160 | | | | | |
| aat | aat | att | cat | gaa | atg | gaa | ata | cag | ctg | aaa | gat | gct | ctg | gag | aaa | 824 |
| Asn | Asn | Ile | His | Glu | Met | Glu | Ile | Gln | Leu | Lys | Asp | Ala | Leu | Glu | Lys | |
| 165 | | | | | 170 | | | | | 175 | | | | | 180 | |
| aat | cag | cag | tgg | ctc | gtg | tat | gat | cag | cag | cgg | gaa | gtc | tat | gta | aaa | 872 |
| Asn | Gln | Gln | Trp | Leu | Val | Tyr | Asp | Gln | Gln | Arg | Glu | Val | Tyr | Val | Lys | |
| | | | 185 | | | | | | 190 | | | | | 195 | | |
| gga | ctt | tta | gca | aag | atc | ttt | gag | ttg | gaa | aag | aaa | acg | gaa | aca | gct | 920 |
| Gly | Leu | Leu | Ala | Lys | Ile | Phe | Glu | Leu | Glu | Lys | Lys | Thr | Glu | Thr | Ala | |
| | | | 200 | | | | | 205 | | | | | 210 | | | |
| gct | cat | tca | ctc | cca | cag | cag | aca | aaa | aag | cct | gaa | tca | gaa | ggg | tat | 968 |
| Ala | His | Ser | Leu | Pro | Gln | Gln | Thr | Lys | Lys | Pro | Glu | Ser | Glu | Gly | Tyr | |
| | | 215 | | | | | 220 | | | | | 225 | | | | |
| ctt | caa | gaa | gag | aag | cag | aaa | tgt | tac | aac | gat | ctc | ttg | gca | agt | gca | 1016 |
| Leu | Gln | Glu | Glu | Lys | Gln | Lys | Cys | Tyr | Asn | Asp | Leu | Leu | Ala | Ser | Ala | |
| | 230 | | | | | 235 | | | | | 240 | | | | | |
| aaa | aaa | gat | ctt | gag | gtt | gaa | cga | caa | acc | ata | act | cag | ctg | agt | ttt | 1064 |
| Lys | Lys | Asp | Leu | Glu | Val | Glu | Arg | Gln | Thr | Ile | Thr | Gln | Leu | Ser | Phe | |
| 245 | | | | | 250 | | | | | 255 | | | | | 260 | |
| gaa | ctg | agt | gaa | ttt | cga | aga | aaa | tat | gaa | gaa | acc | caa | aaa | gaa | gtt | 1112 |
| Glu | Leu | Ser | Glu | Phe | Arg | Arg | Lys | Tyr | Glu | Glu | Thr | Gln | Lys | Glu | Val | |
| | | | 265 | | | | | 270 | | | | | | 275 | | |
| cac | aat | tta | aat | cag | ctg | ttg | tat | tca | caa | aga | agg | gca | gat | gtg | caa | 1160 |
| His | Asn | Leu | Asn | Gln | Leu | Leu | Tyr | Ser | Gln | Arg | Arg | Ala | Asp | Val | Gln | |
| | | 280 | | | | | 285 | | | | | 290 | | | | |
| cat | ctg | gaa | gat | gat | agg | cat | aaa | aca | gag | aag | ata | caa | aaa | ctc | agg | 1208 |
| His | Leu | Glu | Asp | Asp | Arg | His | Lys | Thr | Glu | Lys | Ile | Gln | Lys | Leu | Arg | |
| | | 295 | | | | | 300 | | | | | 305 | | | | |
| gaa | gag | aat | gat | att | gct | agg | gga | aaa | ctt | gaa | gaa | gag | aag | aag | aga | 1256 |
| Glu | Glu | Asn | Asp | Ile | Ala | Arg | Gly | Lys | Leu | Glu | Glu | Glu | Lys | Lys | Arg | |
| | 310 | | | | | 315 | | | | | 320 | | | | | |
| tcc | gaa | gag | ctc | tta | tct | cag | gtc | cag | ttt | ctt | tac | aca | tct | ctg | cta | 1304 |
| Ser | Glu | Glu | Leu | Leu | Ser | Gln | Val | Gln | Phe | Leu | Tyr | Thr | Ser | Leu | Leu | |
| | 325 | | | | 330 | | | | 335 | | | | | | 340 | |
| aag | cag | caa | gaa | gaa | caa | aca | agg | gta | gct | ctg | ttg | gaa | caa | cag | atg | 1352 |
| Lys | Gln | Gln | Glu | Glu | Gln | Thr | Arg | Val | Ala | Leu | Leu | Glu | Gln | Gln | Met | |
| | | | 345 | | | | | 350 | | | | | | 355 | | |
| cag | gca | tgt | act | tta | gac | ttt | gaa | aat | gaa | aaa | ctc | gac | cgt | caa | cat | 1400 |
| Gln | Ala | Cys | Thr | Leu | Asp | Phe | Glu | Asn | Glu | Lys | Leu | Asp | Arg | Gln | His | |

| 360 | 365 | 370 | |
|---|-----|-----|------|
| gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga | | | 1448 |
| Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg | | | |
| 375 | 380 | 385 | |
| aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc | | | 1496 |
| Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Glu Leu His Glu Phe Ala | | | |
| 390 | 395 | 400 | |
| atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa | | | 1544 |
| Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu | | | |
| 405 | 410 | 415 | 420 |
| aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc | | | 1592 |
| Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser | | | |
| 425 | 430 | 435 | |
| ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat | | | 1640 |
| Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His | | | |
| 440 | 445 | 450 | |
| cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt | | | 1689 |
| Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys | | | |
| 455 | 460 | | |
| atttgttttg atattaaaag attcaatact gtattttctg ttagcttggtg ggcattttga | | | 1749 |
| attatatatt tcacattttg cataaaaactg cctatctacc tttgacactc cagcatgcta | | | 1809 |
| gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgtatc ctccctgaca | | | 1869 |
| tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg agactactaa | | | 1929 |
| cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcagggttatt gctaattgggt | | | 1989 |
| taatgcacca gcaagcaaaa tatttttatgt tttggggggt tgaaaaatca aagataatta | | | 2049 |
| accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac ctacaatcct | | | 2109 |
| aattttgatg tccattgtta agagggtgtg atagatacta tttttttttt catattgtat | | | 2169 |
| agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac cattgaaact | | | 2229 |
| taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt ttgaggcata | | | 2289 |
| atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac tgtaacttga | | | 2349 |
| attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat aaacccatgt | | | 2409 |
| agccctctca tttgattgac agtatttttag ttatttttgg cattcttaaa gctgggcaat | | | 2469 |
| gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt ttgtaaacca | | | 2529 |
| aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac tgtaaatgag | | | 2589 |
| aaaagaataa aattatttaa tgttttaaaa aaaaaaaaaa aaaaaa | | | 2635 |

<210> 228

<211> 464

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<212> PRT

<213> homo sapiens

<400> 228

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Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
35 40 45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
50 55 60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65 70 75 80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
85 90 95

Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
100 105 110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
115 120 125

Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
130 135 140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145 150 155 160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
165 170 175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
180 185 190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
195 200 205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
210 215 220

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Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225 230 235 240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
245 250 255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
260 265 270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
275 280 285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
290 295 300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305 310 315 320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
325 330 335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
340 345 350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
355 360 365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu
370 375 380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385 390 395 400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
405 410 415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
420 425 430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
435 440 445

Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
450 455 460

<210> 229

<211> 2635

<212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (285) .. (1679)

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 gggagggcag gtcagtgggc agatcgcgtc cgcgggattc aatctctgcc cgctctgata 180
 acagtccttt tccctggcgc tcacttcgtg cctggcaccg ggctgggagc ctcaagaccg 240
 ttgtctcttc gatcgcttct ttggacttgg cgaccatttc agag atg tct tcc aga 296
 Met Ser Ser Arg
 1
 agt acc aaa gat tta att aaa agt aag tgg gga tgc aag cct agt aac 344
 Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys Pro Ser Asn
 5 10 15 20
 tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa att gca cac 392
 Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu Ile Ala His
 25 30 35
 tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga aag ctg act 440
 Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly Lys Leu Thr
 40 45 50
 gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc ctt gag gct 488
 Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val Leu Glu Ala
 55 60 65
 gag aag gag aag aat gct tat caa ctc aca gag aag gac aaa gaa ata 536
 Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp Lys Glu Ile
 70 75 80
 cag cga ctg aga gac caa ctg aag gcc aga tat agt act acc gca ttg 584
 Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr Thr Ala Leu
 85 90 95 100
 ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg agg gag cag 632
 Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg Arg Glu Gln
 105 110 115
 gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa caa cag ttg 680
 Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys Gln Gln Leu
 120 125 130
 tct gct gca acc tca cga att gct gaa ctt gaa agc aaa acc aat aca 728
 Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys Thr Asn Thr
 135 140 145
 ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac tca tca ata 776
 Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn Ser Ser Ile
 150 155 160

| | |
|---|------|
| aat aat att cat gaa atg gaa ata cag ctg aaa gat gct ctg gag aaa | 824 |
| Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala Leu Glu Lys | |
| 165 170 175 180 | |
| aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc tat gta aaa | 872 |
| Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val Tyr Val Lys | |
| 185 190 195 | |
| gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg gaa aca gct | 920 |
| Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr Glu Thr Ala | |
| 200 205 210 | |
| gct cat tca ctc cca cag cag aca aaa aag cct gaa tca gaa ggt tat | 968 |
| Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser Glu Gly Tyr | |
| 215 220 225 | |
| ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg gca agt gca | 1016 |
| Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu Ala Ser Ala | |
| 230 235 240 | |
| aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag ctg agt ttt | 1064 |
| Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln Leu Ser Phe | |
| 245 250 255 260 | |
| gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa aaa gaa gtt | 1112 |
| Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln Lys Glu Val | |
| 265 270 275 | |
| cac aat tta aat cag ctg ttg tat tca caa aga agg gca gat gtg caa | 1160 |
| His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala Asp Val Gln | |
| 280 285 290 | |
| cat ctg gaa gat gat agg cat aaa aca gag aag ata caa aaa ctc agg | 1208 |
| His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln Lys Leu Arg | |
| 295 300 305 | |
| gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag aag aag aga | 1256 |
| Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu Lys Lys Arg | |
| 310 315 320 | |
| tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca tct ctg cta | 1304 |
| Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr Ser Leu Leu | |
| 325 330 335 340 | |
| aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa caa cag atg | 1352 |
| Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu Gln Gln Met | |
| 345 350 355 | |
| cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac cgt caa cat | 1400 |
| Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp Arg Gln His | |
| 360 365 370 | |
| gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga | 1448 |
| Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg | |
| 375 380 385 | |
| aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc | 1496 |
| Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His Glu Phe Ala | |
| 390 395 400 | |
| atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa | 1544 |

Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu
 405 410 415 420

aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc 1592
 Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser
 425 430 435

ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat 1640
 Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His
 440 445 450

cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt 1689
 Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
 455 460

atttgttttg atattaaaag attcaatact gtattttctg ttagcttggtg ggcattttga 1749

attatatatt tcacattttg cataaaactg cctatctacc tttgacactc cagcatgcta 1809

gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgtatc ctccctgaca 1869

tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg agactactaa 1929

cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt gctaattgggt 1989

taatgcacca gcaagcaaaa tatttttatgt tttgggggtt tgaaaaatca aagataatta 2049

accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac ctacaatcct 2109

aattttgatg tccattgtta agagggtggtg atagatacta tttttttttt catattgtat 2169

agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac cattgaaact 2229

taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt ttgaggcata 2289

atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac tgtaacttga 2349

attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat aaacccatgt 2409

agccctctca tttgattgac agtatttttag ttatttttgg cattcttaaa gctgggcaat 2469

gtaatgatca gatctttggt tgtctgaaca ggtattttta tacatgcttt ttgtaaacca 2529

aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac tgtaaatgag 2589

aaaagaataa aattatttaa tgttttataa aaaaaaaaaa aaaaaa 2635

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<211> 464

<212> PRT

<400> 230

Met Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser
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Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
35 40 45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
50 55 60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65 70 75 80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
85 90 95

Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
100 105 110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
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Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
130 135 140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145 150 155 160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
165 170 175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
180 185 190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
195 200 205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
210 215 220

Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225 230 235 240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
245 250 255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
260 265 270

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Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
275 280 285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
290 295 300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
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Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
325 330 335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
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Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
355 360 365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu
370 375 380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385 390 395 400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
405 410 415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
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Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
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| Met Leu Arg Val Ile Val Glu Ser | |
| 1 5 | |
| gcc agc aat atc cct aaa acg aaa ttt ggc aag ccg gat cct att gtt | 160 |
| Ala Ser Asn Ile Pro Lys Thr Lys Phe Gly Lys Pro Asp Pro Ile Val | |
| 10 15 20 | |
| tct gtc att ttt aag gat gag aaa aag aaa aca aag aaa gtt gat aat | 208 |
| Ser Val Ile Phe Lys Asp Glu Lys Lys Lys Thr Lys Lys Val Asp Asn | |
| 25 30 35 40 | |
| gaa ttg aac cct gtc tgg aat gag att ttg gag ttt gac ttg agg ggt | 256 |
| Glu Leu Asn Pro Val Trp Asn Glu Ile Leu Glu Phe Asp Leu Arg Gly | |
| 45 50 55 | |
| ata cca ctg gac ttt tca tct tcc ctt ggg att att gtg aaa gat ttt | 304 |
| Ile Pro Leu Asp Phe Ser Ser Ser Leu Gly Ile Ile Val Lys Asp Phe | |
| 60 65 70 | |
| gag aca att gga caa aat aaa tta att ggc acg gcg act gta gcc ctg | 352 |
| Glu Thr Ile Gly Gln Asn Lys Leu Ile Gly Thr Ala Thr Val Ala Leu | |
| 75 80 85 | |
| aag gac ctg act ggt gac cag agc aga tcc ctg ccg tac aag ctg atc | 400 |
| Lys Asp Leu Thr Gly Asp Gln Ser Arg Ser Leu Pro Tyr Lys Leu Ile | |
| 90 95 100 | |
| tcc ctg cta aat gaa aaa ggg caa gat act ggg gcc acc att gac ttg | 448 |
| Ser Leu Leu Asn Glu Lys Gly Gln Asp Thr Gly Ala Thr Ile Asp Leu | |
| 105 110 115 120 | |
| gtg atc ggc tat gat ccg cct tct gct cca cat cca aat gac ctg agc | 496 |
| Val Ile Gly Tyr Asp Pro Pro Ser Ala Pro His Pro Asn Asp Leu Ser | |
| 125 130 135 | |
| ggg ccc agc gtg cca ggc atg gga gga gat ggg gaa gaa gat gaa ggt | 544 |
| Gly Pro Ser Val Pro Gly Met Gly Gly Asp Gly Glu Glu Asp Glu Gly | |
| 140 145 150 | |
| gat gaa gac agg ttg gac aat gca gtc agg ggc cct ggg ccc aag ggg | 592 |
| Asp Glu Asp Arg Leu Asp Asn Ala Val Arg Gly Pro Gly Pro Lys Gly | |
| 155 160 165 | |
| cca gtt ggg acg gtg tcg gaa gct cag ctt gct cgg agg ctc acc aaa | 640 |
| Pro Val Gly Thr Val Ser Glu Ala Gln Leu Ala Arg Arg Leu Thr Lys | |
| 170 175 180 | |
| gta aag aac agc cgg cgg atg ctg tca aat aag cca cag gac ttc cag | 688 |
| Val Lys Asn Ser Arg Arg Met Leu Ser Asn Lys Pro Gln Asp Phe Gln | |
| 185 190 195 200 | |
| atc cgc gtc cga gtg att gag ggc cga cag tta agt ggt aac aac ata | 736 |
| Ile Arg Val Arg Val Ile Glu Gly Arg Gln Leu Ser Gly Asn Asn Ile | |
| 205 210 215 | |
| agg cct gtg gtc aaa gtt cac gtc tgt ggc cag aca cac cga aca aga | 784 |
| Arg Pro Val Val Lys Val His Val Cys Gly Gln Thr His Arg Thr Arg | |
| 220 225 230 | |
| atc aag aga gga aac aac cct ttt ttt gat gag ttg ttt ttc tac aat | 832 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Ile | Lys | Arg | Gly | Asn | Asn | Pro | Phe | Phe | Asp | Glu | Leu | Phe | Phe | Tyr | Asn | | |
| | | 235 | | | | | 240 | | | | | 245 | | | | | |
| gtc | aac | atg | acc | cct | tct | gaa | ttg | atg | gat | gag | atc | atc | agc | atc | cgg | | 880 |
| Val | Asn | Met | Thr | Pro | Ser | Glu | Leu | Met | Asp | Glu | Ile | Ile | Ser | Ile | Arg | | |
| | 250 | | | | | 255 | | | | | 260 | | | | | | |
| gtt | tat | aat | tct | cac | tct | ctg | cgg | gca | gat | tgt | ctg | atg | ggg | gaa | ttt | | 928 |
| Val | Tyr | Asn | Ser | His | Ser | Leu | Arg | Ala | Asp | Cys | Leu | Met | Gly | Glu | Phe | | |
| | 265 | | | | 270 | | | | | 275 | | | | | 280 | | |
| aag | att | gat | gtt | gga | ttt | gtt | tat | gat | gaa | cct | ggc | cat | gct | gtc | atg | | 976 |
| Lys | Ile | Asp | Val | Gly | Phe | Val | Tyr | Asp | Glu | Pro | Gly | His | Ala | Val | Met | | |
| | | | | 285 | | | | | 290 | | | | | 295 | | | |
| aga | aag | tgg | ctt | ctt | ctc | aat | gac | ccg | gaa | gat | acc | agt | tca | ggg | tct | | 1024 |
| Arg | Lys | Trp | Leu | Leu | Leu | Asn | Asp | Pro | Glu | Asp | Thr | Ser | Ser | Gly | Ser | | |
| | | | 300 | | | | | 305 | | | | | 310 | | | | |
| aaa | ggg | tat | atg | aaa | gtc | agc | atg | ttt | gtc | ctg | gga | acc | gga | gat | gag | | 1072 |
| Lys | Gly | Tyr | Met | Lys | Val | Ser | Met | Phe | Val | Leu | Gly | Thr | Gly | Asp | Glu | | |
| | | 315 | | | | | 320 | | | | | 325 | | | | | |
| cct | cct | cct | gag | aga | cga | gat | cgt | gat | aat | gac | agt | gat | gat | gtg | gag | | 1120 |
| Pro | Pro | Pro | Glu | Arg | Arg | Asp | Arg | Asp | Asn | Asp | Ser | Asp | Asp | Val | Glu | | |
| | | | 330 | | | 335 | | | | | | 340 | | | | | |
| agt | aat | ttg | tta | ctc | cct | gct | ggc | att | gcc | ctc | cgg | tgg | gtg | acc | ttc | | 1168 |
| Ser | Asn | Leu | Leu | Leu | Pro | Ala | Gly | Ile | Ala | Leu | Arg | Trp | Val | Thr | Phe | | |
| | | | | | 350 | | | | | 355 | | | | | 360 | | |
| ttg | ctg | aaa | atc | tac | cga | gct | gag | gac | atc | ccc | cag | atg | gat | gat | gcc | | 1216 |
| Leu | Leu | Lys | Ile | Tyr | Arg | Ala | Glu | Asp | Ile | Pro | Gln | Met | Asp | Asp | Ala | | |
| | | | | 365 | | | | | 370 | | | | | | 375 | | |
| ttc | tca | cag | aca | gta | aag | gaa | ata | ttt | gga | ggc | aat | gca | gat | aag | aaa | | 1264 |
| Phe | Ser | Gln | Thr | Val | Lys | Glu | Ile | Phe | Gly | Gly | Asn | Ala | Asp | Lys | Lys | | |
| | | | 380 | | | | | 385 | | | | | 390 | | | | |
| aat | ctc | gtg | gat | cct | ttt | gta | gaa | gtt | tcc | ttt | gct | gga | aaa | aag | gtt | | 1312 |
| Asn | Leu | Val | Asp | Pro | Phe | Val | Glu | Val | Ser | Phe | Ala | Gly | Lys | Lys | Val | | |
| | | | 395 | | | | 400 | | | | | 405 | | | | | |
| tgt | aca | aac | ata | att | gag | aaa | aat | gca | aac | cca | gag | tgg | aat | cag | gtc | | 1360 |
| Cys | Thr | Asn | Ile | Ile | Glu | Lys | Asn | Ala | Asn | Pro | Glu | Trp | Asn | Gln | Val | | |
| | 410 | | | | | 415 | | | | | 420 | | | | | | |
| gtc | aat | ctt | cag | atc | aag | ttt | cct | tca | gtg | tgt | gaa | aaa | ata | aaa | cta | | 1408 |
| Val | Asn | Leu | Gln | Ile | Lys | Phe | Pro | Ser | Val | Cys | Glu | Lys | Ile | Lys | Leu | | |
| | 425 | | | | 430 | | | | | 435 | | | | | 440 | | |
| aca | ata | tat | gac | tgg | gac | cgt | ctt | act | aaa | aat | gat | gta | gtt | gga | aca | | 1456 |
| Thr | Ile | Tyr | Asp | Trp | Asp | Arg | Leu | Thr | Lys | Asn | Asp | Val | Val | Gly | Thr | | |
| | | | | 445 | | | | | 450 | | | | | 455 | | | |
| aca | tat | cta | cac | ctc | tct | aaa | att | gct | gcc | tct | ggg | ggg | gaa | gtg | gaa | | 1504 |
| Thr | Tyr | Leu | His | Leu | Ser | Lys | Ile | Ala | Ala | Ser | Gly | Gly | Glu | Val | Glu | | |
| | | | 460 | | | | | 465 | | | | | 470 | | | | |
| gat | ttc | tca | tct | tcg | gga | act | ggg | gct | gca | tca | tat | aca | gta | aac | aca | | 1552 |
| Asp | Phe | Ser | Ser | Ser | Gly | Thr | Gly | Ala | Ala | Ser | Tyr | Thr | Val | Asn | Thr | | |

| 475 | 480 | 485 | |
|---|-----|-----|------|
| gga gaa aca gag gta ggc ttt gtt cca acg ttt gga cct tgt tac ctg Gly Glu Thr Glu Val Gly Phe Val Pro Thr Phe Gly Pro Cys Tyr Leu 490 495 500 | | | 1600 |
| aat ctt tat gga agc ccc agg gag tac acg gga ttc cca gac ccc tat Asn Leu Tyr Gly Ser Pro Arg Glu Tyr Thr Gly Phe Pro Asp Pro Tyr 505 510 515 520 | | | 1648 |
| gat gag ctg aat act gga aag ggg gaa gga gtt gcc tac aga ggc agg Asp Glu Leu Asn Thr Gly Lys Gly Glu Gly Val Ala Tyr Arg Gly Arg 525 530 535 | | | 1696 |
| atc ttg gtt gaa tta gcc act ttt ctt gag aag aca cca cca gat aaa Ile Leu Val Glu Leu Ala Thr Phe Leu Glu Lys Thr Pro Pro Asp Lys 540 545 550 | | | 1744 |
| aag ctt gag ccc att tca aat gat gac ctg ctg gtt gtt gag aaa tac Lys Leu Glu Pro Ile Ser Asn Asp Asp Leu Leu Val Val Glu Lys Tyr 555 560 565 | | | 1792 |
| cag cga agg cgg aag tac agc ctg tct gcc gtg ttt cat tca gcc acc Gln Arg Arg Arg Lys Tyr Ser Leu Ser Ala Val Phe His Ser Ala Thr 570 575 580 | | | 1840 |
| atg ttg caa gat gtt ggt gag gcc att cag ttt gaa gtc agc att ggg Met Leu Gln Asp Val Gly Glu Ala Ile Gln Phe Glu Val Ser Ile Glu 585 590 595 600 | | | 1888 |
| aac tat ggc aac aag ttt gac acc acc tgt aag cct ttg gca tca aca Asn Tyr Gly Asn Lys Phe Asp Thr Thr Cys Lys Pro Leu Ala Ser Thr 605 610 615 | | | 1936 |
| act cag tac agc cgt gct gta ttt gat ggc aac tac tat tat tac ttg Thr Gln Tyr Ser Arg Ala Val Phe Asp Gly Asn Tyr Tyr Tyr Tyr Leu 620 625 630 | | | 1984 |
| cct tgg gcc cac acc aag cca gtt gtt acc ctg act tca tac tgg gag Pro Trp Ala His Thr Lys Pro Val Val Thr Leu Thr Ser Tyr Trp Glu 635 640 645 | | | 2032 |
| gat att agt cat cgc ctg gat gcg gtg aac act ctc cta gct atg gca Asp Ile Ser His Arg Leu Asp Ala Val Asn Thr Leu Leu Ala Met Ala 650 655 660 | | | 2080 |
| gaa cgg ctg caa aca aat ata gaa gct cta aaa tca ggg ata caa ggt Glu Arg Leu Gln Thr Asn Ile Glu Ala Leu Lys Ser Gly Ile Gln Gly 665 670 675 680 | | | 2128 |
| aaa att cct gca aac cag ctg gct gaa ttg tgg ctg aag ctg ata gat Lys Ile Pro Ala Asn Gln Leu Ala Glu Leu Trp Leu Lys Leu Ile Asp 685 690 695 | | | 2176 |
| gaa gtt ata gaa gac acg aga tac acg ttg cct ctc aca gaa gga aaa Glu Val Ile Glu Asp Thr Arg Tyr Thr Leu Pro Leu Thr Glu Gly Lys 700 705 710 | | | 2224 |
| gcc aac gtc aca gtt ctc gat act cag atc cga aag ctg cgg tcc agg Ala Asn Val Thr Val Leu Asp Thr Gln Ile Arg Lys Leu Arg Ser Arg 715 720 725 | | | 2272 |

| | |
|---|------|
| tct ctc tcc caa ata cat gag gcg gct gtg agg atg agg tcg gaa gcc | 2320 |
| Ser Leu Ser Gln Ile His Glu Ala Ala Val Arg Met Arg Ser Glu Ala | |
| 730 735 740 | |
| aca gat gtg aag tcc aca ctg gca gaa att gag gac tgg ctt gat aaa | 2368 |
| Thr Asp Val Lys Ser Thr Leu Ala Glu Ile Glu Asp Trp Leu Asp Lys | |
| 745 750 755 760 | |
| tta atg cag ctg act gaa gag cca cag aac agc atg cct gac atc atc | 2416 |
| Leu Met Gln Leu Thr Glu Glu Pro Gln Asn Ser Met Pro Asp Ile Ile | |
| 765 770 775 | |
| atc tgg atg atc cgg gga gag aag aga ctg gcc tat gca cga att ccc | 2464 |
| Ile Trp Met Ile Arg Gly Glu Lys Arg Leu Ala Tyr Ala Arg Ile Pro | |
| 780 785 790 | |
| gca cat cag gtc ttg tac tcc acc agt ggt gag aat gca tct gga aaa | 2512 |
| Ala His Gln Val Leu Tyr Ser Thr Ser Gly Glu Asn Ala Ser Gly Lys | |
| 795 800 805 | |
| tac tgt ggg aaa acc caa acc atc ttt ctg aag tat cca cag gag aaa | 2560 |
| Tyr Cys Gly Lys Thr Gln Thr Ile Phe Leu Lys Tyr Pro Gln Glu Lys | |
| 810 815 820 | |
| aac aac ggg cca aag gtg cct gtg gag ttg cga gtg aac atc tgg cta | 2608 |
| Asn Asn Gly Pro Lys Val Pro Val Glu Leu Arg Val Asn Ile Trp Leu | |
| 825 830 835 840 | |
| ggc tta agt gct gtg gag aag aag ttt aac agc ttc gca gaa gga act | 2656 |
| Gly Leu Ser Ala Val Glu Lys Lys Phe Asn Ser Phe Ala Glu Gly Thr | |
| 845 850 855 | |
| ttc acc gtc ttt gct gaa atg tat gaa aat caa gct ctc atg ttt gga | 2704 |
| Phe Thr Val Phe Ala Glu Met Tyr Glu Asn Gln Ala Leu Met Phe Gly | |
| 860 865 870 | |
| aaa tgg ggt act tct gga tta gta gga cgt cat aag ttt tct gat gtc | 2752 |
| Lys Trp Gly Thr Ser Gly Leu Val Gly Arg His Lys Phe Ser Asp Val | |
| 875 880 885 | |
| aca gga aaa ata aaa ctc aag agg gaa ttt ttt ctg cct cca aaa ggc | 2800 |
| Thr Gly Lys Ile Lys Leu Lys Arg Glu Phe Phe Leu Pro Pro Lys Gly | |
| 890 895 900 | |
| tgg gaa tgg gaa gga gag tgg ata gtt gat cct gaa aga agc ttg ctg | 2848 |
| Trp Glu Trp Glu Gly Glu Trp Ile Val Asp Pro Glu Arg Ser Leu Leu | |
| 905 910 915 920 | |
| act gag gca gat gca ggt cac acg gag ttc act gat gaa gtc tat cag | 2896 |
| Thr Glu Ala Asp Ala Gly His Thr Glu Phe Thr Asp Glu Val Tyr Gln | |
| 925 930 935 | |
| aac gag agc cgc tac ccc ggg ggc gac tgg aag ccg gcc gag gac acc | 2944 |
| Asn Glu Ser Arg Tyr Pro Gly Gly Asp Trp Lys Pro Ala Glu Asp Thr | |
| 940 945 950 | |
| tac acg gat gcg aac ggc gat aaa gca gca tca ccc agc gag ttg act | 2992 |
| Tyr Thr Asp Ala Asn Gly Asp Lys Ala Ala Ser Pro Ser Glu Leu Thr | |
| 955 960 965 | |

| | |
|---|------|
| tgt cct cca ggt tgg gaa tgg gaa gat gat gca tgg tct tat gac ata | 3040 |
| Cys Pro Pro Gly Trp Glu Trp Glu Asp Asp Ala Trp Ser Tyr Asp Ile | |
| 970 975 980 | |
| aat cga gcg gtg gat gag aaa ggc tgg gaa tat gga atc acc att cct | 3088 |
| Asn Arg Ala Val Asp Glu Lys Gly Trp Glu Tyr Gly Ile Thr Ile Pro | |
| 985 990 995 1000 | |
| cct gat cat aag ccc aaa tcc tgg gtt gca gca gag aaa atg tac | 3133 |
| Pro Asp His Lys Pro Lys Ser Trp Val Ala Ala Glu Lys Met Tyr | |
| 1005 1010 1015 | |
| cac act cat aga cgg cga agg ctg gtc cga aaa cgc aag aaa gat | 3178 |
| His Thr His Arg Arg Arg Arg Leu Val Arg Lys Arg Lys Lys Asp | |
| 1020 1025 1030 | |
| tta aca cag act gct tca agc acc gca agg gcc atg gag gaa ttg | 3223 |
| Leu Thr Gln Thr Ala Ser Ser Thr Ala Arg Ala Met Glu Glu Leu | |
| 1035 1040 1045 | |
| caa gac caa gag ggc tgg gaa tat gct tct cta att ggc tgg aaa | 3268 |
| Gln Asp Gln Glu Gly Trp Glu Tyr Ala Ser Leu Ile Gly Trp Lys | |
| 1050 1055 1060 | |
| ttt cac tgg aaa caa cgt agt tca gat acc ttc cgc cgc aga cgc | 3313 |
| Phe His Trp Lys Gln Arg Ser Ser Asp Thr Phe Arg Arg Arg Arg | |
| 1065 1070 1075 | |
| tgg agg aga aaa atg gct cct tca gaa aca cat ggt gca gct gcc | 3358 |
| Trp Arg Arg Lys Met Ala Pro Ser Glu Thr His Gly Ala Ala Ala | |
| 1080 1085 1090 | |
| atc ttt aaa ctt gaa ggt gcc ctt ggg gca gac act acc gaa gat | 3403 |
| Ile Phe Lys Leu Glu Gly Ala Leu Gly Ala Asp Thr Thr Glu Asp | |
| 1095 1100 1105 | |
| ggg gat gag aag agc ctg gag aaa cag aag cac agt gcc acc act | 3448 |
| Gly Asp Glu Lys Ser Leu Glu Lys Gln Lys His Ser Ala Thr Thr | |
| 1110 1115 1120 | |
| gtg ttc gga gca aac acc ccc att gtt tcc tgc aat ttt gac aga | 3493 |
| Val Phe Gly Ala Asn Thr Pro Ile Val Ser Cys Asn Phe Asp Arg | |
| 1125 1130 1135 | |
| gtc tac atc tac cat ctg cgc tgc tat gtc tat caa gcc aga aac | 3538 |
| Val Tyr Ile Tyr His Leu Arg Cys Tyr Val Tyr Gln Ala Arg Asn | |
| 1140 1145 1150 | |
| ctc ttg gct tta gat aag gat agc ttt tca gat cca tat gct cat | 3583 |
| Leu Leu Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Tyr Ala His | |
| 1155 1160 1165 | |
| atc tgt ttc ctc cat cgg agc aaa acc act gag atc atc cat tca | 3628 |
| Ile Cys Phe Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser | |
| 1170 1175 1180 | |
| acc ctg aat ccc acg tgg gac caa aca att ata ttc gat gaa gtt | 3673 |
| Thr Leu Asn Pro Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val | |
| 1185 1190 1195 | |
| gaa atc tat ggg gaa ccc caa aca gtt cta cag aat cca ccc aaa | 3718 |

| | | | | |
|---------------------|---------------------|---------------------|---------------------|------|
| Glu Ile Tyr Gly | Glu | Pro Gln Thr Val Leu | Gln Asn Pro Pro Lys | |
| | 1200 | | 1205 | 1210 |
| gtt atc atg gaa ctt | ttt gac aat gac caa | gtg ggc aaa gat gaa | 3763 | |
| Val Ile Met Glu Leu | Phe Asp Asn Asp Gln | Val Gly Lys Asp Glu | | |
| | 1215 | 1220 | 1225 | |
| ttt tta gga cga agc | att ttc tct cct gtg | gtg aaa ctg aac tca | 3808 | |
| Phe Leu Gly Arg Ser | Ile Phe Ser Pro Val | Val Lys Leu Asn Ser | | |
| | 1230 | 1235 | 1240 | |
| gaa atg gac atc aca | ccc aaa ctt ctc tgg | cac cca gta atg aat | 3853 | |
| Glu Met Asp Ile Thr | Pro Lys Leu Leu Trp | His Pro Val Met Asn | | |
| | 1245 | 1250 | 1255 | |
| gga gac aaa gcc tgc | ggg gat gtt ctt gta | act gca gag ctg att | 3898 | |
| Gly Asp Lys Ala Cys | Gly Asp Val Leu Val | Thr Ala Glu Leu Ile | | |
| | 1260 | 1265 | 1270 | |
| ctg agg ggc aag gat | ggc tcc aac ctt ccc | att ctt ccc cct caa | 3943 | |
| Leu Arg Gly Lys Asp | Gly Ser Asn Leu Pro | Ile Leu Pro Pro Gln | | |
| | 1275 | 1280 | 1285 | |
| agg gcg cca aat cta | tac atg gtc ccc cag | ggg atc agg cct gtg | 3988 | |
| Arg Ala Pro Asn Leu | Tyr Met Val Pro Gln | Gly Ile Arg Pro Val | | |
| | 1290 | 1295 | 1300 | |
| gtc cag ctc act gcc | att gag att cta gct | tgg ggc tta aga aat | 4033 | |
| Val Gln Leu Thr Ala | Ile Glu Ile Leu Ala | Trp Gly Leu Arg Asn | | |
| | 1305 | 1310 | 1315 | |
| atg aaa aac ttc cag | atg gct tct atc aca | tcc ccc agt ctt gtt | 4078 | |
| Met Lys Asn Phe Gln | Met Ala Ser Ile Thr | Ser Pro Ser Leu Val | | |
| | 1320 | 1325 | 1330 | |
| gtg gag tgt gga gga | gaa agg gtg gaa tcg | gtg gtg atc aaa aac | 4123 | |
| Val Glu Cys Gly Gly | Glu Arg Val Glu Ser | Val Val Ile Lys Asn | | |
| | 1335 | 1340 | 1345 | |
| ctt aag aag aca ccc | aac ttt cca agt tct | gtt ctc ttc atg aaa | 4168 | |
| Leu Lys Lys Thr Pro | Asn Phe Pro Ser Ser | Val Leu Phe Met Lys | | |
| | 1350 | 1355 | 1360 | |
| gtg ttc ttg ccc aag | gag gaa ttg tac atg | ccc cca ctg gtg atc | 4213 | |
| Val Phe Leu Pro Lys | Glu Glu Leu Tyr Met | Pro Pro Leu Val Ile | | |
| | 1365 | 1370 | 1375 | |
| aag gtc atc gac cac | agg cag ttt ggg cgg | aag cct gtc gtc ggc | 4258 | |
| Lys Val Ile Asp His | Arg Gln Phe Gly Arg | Lys Pro Val Val Gly | | |
| | 1380 | 1385 | 1390 | |
| cag tgc acc atc gag | cgc ctg gac cgc ttt | cgc tgt gac cct tat | 4303 | |
| Gln Cys Thr Ile Glu | Arg Leu Asp Arg Phe | Arg Cys Asp Pro Tyr | | |
| | 1395 | 1400 | 1405 | |
| gca ggg aaa gag gac | atc gtc cca cag ctc | aaa gcc tcc ctt ctg | 4348 | |
| Ala Gly Lys Glu Asp | Ile Val Pro Gln Leu | Lys Ala Ser Leu Leu | | |
| | 1410 | 1415 | 1420 | |
| tct gcc cca cca tgc | cgg gac atc gtt atc | gaa atg gaa gac acc | 4393 | |
| Ser Ala Pro Pro Cys | Arg Asp Ile Val Ile | Glu Met Glu Asp Thr | | |

| 1425 | 1430 | 1435 | |
|--|--|--|------|
| aaa cca tta ctg gct Lys Pro Leu Leu Ala 1440 | tct aag ctg aca gaa Ser Lys Leu Thr Glu 1445 | aag gag gaa gaa atc Lys Glu Glu Glu Ile 1450 | 4438 |
| gtg gac tgg tgg agt Val Asp Trp Trp Ser 1455 | aaa ttt tat gct tcc Lys Phe Tyr Ala Ser 1460 | tca ggg gaa cat gaa Ser Gly Glu His Glu 1465 | 4483 |
| aaa tgc gga cag tat Lys Cys Gly Gln Tyr 1470 | att cag aaa ggc tat Ile Gln Lys Gly Tyr 1475 | tcc aag ctc aag ata Ser Lys Leu Lys Ile 1480 | 4528 |
| tat aat tgt gaa cta Tyr Asn Cys Glu Leu 1485 | gaa aat gta gca gaa Glu Asn Val Ala Glu 1490 | ttt gag ggc ctg aca Phe Glu Gly Leu Thr 1495 | 4573 |
| gac ttc tca gat acg Asp Phe Ser Asp Thr 1500 | ttc aag ttg tac cga Phe Lys Leu Tyr Arg 1505 | ggc aag tcg gat gaa Gly Lys Ser Asp Glu 1510 | 4618 |
| aat gaa gat cct tct Asn Glu Asp Pro Ser 1515 | gtg gtt gga gag ttt Val Val Gly Glu Phe 1520 | aag ggc tcc ttt cgg Lys Gly Ser Phe Arg 1525 | 4663 |
| atc tac cct ctg ccg Ile Tyr Pro Leu Pro 1530 | gat gac ccc agc gtg Asp Asp Pro Ser Val 1535 | cca gcc cct ccc aga Pro Ala Pro Pro Arg 1540 | 4708 |
| cag ttt cgg gaa tta Gln Phe Arg Glu Leu 1545 | cct gac agc gtc cca Pro Asp Ser Val Pro 1550 | cag gaa tgc acg gtt Gln Glu Cys Thr Val 1555 | 4753 |
| agg att tac att gtt Arg Ile Tyr Ile Val 1560 | cga ggc tta gag ctc Arg Gly Leu Glu Leu 1565 | cag ccc cag gac aac Gln Pro Gln Asp Asn 1570 | 4798 |
| aat ggc ctg tgt gac Asn Gly Leu Cys Asp 1575 | cct tac ata aaa ata Pro Tyr Ile Lys Ile 1580 | aca ctg ggc aaa aaa Thr Leu Gly Lys Lys 1585 | 4843 |
| gtc att gaa gac cga Val Ile Glu Asp Arg 1590 | gat cac tac att ccc Asp His Tyr Ile Pro 1595 | aac act ctc aac cca Asn Thr Leu Asn Pro 1600 | 4888 |
| gtc ttt ggc agg atg Val Phe Gly Arg Met 1605 | tac gaa ctg agc tgc Tyr Glu Leu Ser Cys 1610 | tac tta cct caa gaa Tyr Leu Pro Gln Glu 1615 | 4933 |
| aaa gac ctg aaa att Lys Asp Leu Lys Ile 1620 | tct gtc tat gat tat Ser Val Tyr Asp Tyr 1625 | gac acc ttt acc cgg Asp Thr Phe Thr Arg 1630 | 4978 |
| gat gaa aaa gta gga Asp Glu Lys Val Gly 1635 | gaa aca att att gat Glu Thr Ile Ile Asp 1640 | ctg gaa aac cga ttc Leu Glu Asn Arg Phe 1645 | 5023 |
| ctt tcc cgc ttt ggg Leu Ser Arg Phe Gly 1650 | tcc cac tgc ggc ata Ser His Cys Gly Ile 1655 | cca gag gag tac tgt Pro Glu Glu Tyr Cys 1660 | 5068 |

| | |
|---|------|
| gtt tct gga gtc aat acc tgg cga gat caa ctg aga cca aca cag | 5113 |
| Val Ser Gly Val Asn Thr Trp Arg Asp Gln Leu Arg Pro Thr Gln | |
| 1665 1670 1675 | |
| ctg ctt caa aat gtc gcc aga ttc aaa ggc ttc cca caa ccc atc | 5158 |
| Leu Leu Gln Asn Val Ala Arg Phe Lys Gly Phe Pro Gln Pro Ile | |
| 1680 1685 1690 | |
| ctt tcc gaa gat ggg agt aga atc aga tat gga gga cga gac tac | 5203 |
| Leu Ser Glu Asp Gly Ser Arg Ile Arg Tyr Gly Gly Arg Asp Tyr | |
| 1695 1700 1705 | |
| agc ttg gat gaa ttt gaa gcc aac aaa atc ctg cac cag cac ctc | 5248 |
| Ser Leu Asp Glu Phe Glu Ala Asn Lys Ile Leu His Gln His Leu | |
| 1710 1715 1720 | |
| ggg gcc cct gaa gag cgg ctt gct ctt cac atc ctc agg act cag | 5293 |
| Gly Ala Pro Glu Glu Arg Leu Ala Leu His Ile Leu Arg Thr Gln | |
| 1725 1730 1735 | |
| ggg ctg gtc cct gag cac gtg gaa aca agg act ttg cac agc acc | 5338 |
| Gly Leu Val Pro Glu His Val Glu Thr Arg Thr Leu His Ser Thr | |
| 1740 1745 1750 | |
| ttc cag ccc aac att tcc cag gga aaa ctt cag atg tgg gtg gat | 5383 |
| Phe Gln Pro Asn Ile Ser Gln Gly Lys Leu Gln Met Trp Val Asp | |
| 1755 1760 1765 | |
| gtt ttc ccc aag agt ttg ggg cca cca ggc cct cct ttc aac atc | 5428 |
| Val Phe Pro Lys Ser Leu Gly Pro Pro Gly Pro Pro Phe Asn Ile | |
| 1770 1775 1780 | |
| aca ccc cgg aaa gcc aag aaa tac tac ctg cgt gtg atc atc tgg | 5473 |
| Thr Pro Arg Lys Ala Lys Lys Tyr Tyr Leu Arg Val Ile Ile Trp | |
| 1785 1790 1795 | |
| aac acc aag gac gtt atc ttg gac gag aaa agc atc aca gga gag | 5518 |
| Asn Thr Lys Asp Val Ile Leu Asp Glu Lys Ser Ile Thr Gly Glu | |
| 1800 1805 1810 | |
| gaa atg agt gac atc tac gtc aaa ggc tgg att cct ggc aat gaa | 5563 |
| Glu Met Ser Asp Ile Tyr Val Lys Gly Trp Ile Pro Gly Asn Glu | |
| 1815 1820 1825 | |
| gaa aac aaa cag aaa aca gat gtc cat tac aga tct ttg gat ggt | 5608 |
| Glu Asn Lys Gln Lys Thr Asp Val His Tyr Arg Ser Leu Asp Gly | |
| 1830 1835 1840 | |
| gaa ggg aat ttt aac tgg cga ttt gtt ttc ccg ttt gac tac ctt | 5653 |
| Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Pro Phe Asp Tyr Leu | |
| 1845 1850 1855 | |
| cca gcc gaa caa ctc tgt atc gtt gcg aaa aaa gag cat ttc tgg | 5698 |
| Pro Ala Glu Gln Leu Cys Ile Val Ala Lys Lys Glu His Phe Trp | |
| 1860 1865 1870 | |
| agt att gac caa acg gaa ttt cga atc cca ccc agg ctg atc att | 5743 |
| Ser Ile Asp Gln Thr Glu Phe Arg Ile Pro Pro Arg Leu Ile Ile | |
| 1875 1880 1885 | |

| | |
|--|------|
| cag ata tgg gac aat gac aag ttt tct ctg gat gac tac ttg ggt | 5788 |
| Gln Ile Trp Asp Asn Asp Lys Phe Ser Leu Asp Asp Tyr Leu Gly | |
| 1890 1895 1900 | |
| ttc cta gaa ctt gac ttg cgt cac acg atc att cct gca aaa tca | 5833 |
| Phe Leu Glu Leu Asp Leu Arg His Thr Ile Ile Pro Ala Lys Ser | |
| 1905 1910 1915 | |
| cca gag aaa tgc agg ttg gac atg att ccg gac ctc aaa gcc atg | 5878 |
| Pro Glu Lys Cys Arg Leu Asp Met Ile Pro Asp Leu Lys Ala Met | |
| 1920 1925 1930 | |
| aac ccc ctt aaa gcc aag aca gcc tcc ctc ttt gag cag aag tcc | 5923 |
| Asn Pro Leu Lys Ala Lys Thr Ala Ser Leu Phe Glu Gln Lys Ser | |
| 1935 1940 1945 | |
| atg aaa gga tgg tgg cca tgc tac gca gag aaa gat ggc gcc cgc | 5968 |
| Met Lys Gly Trp Trp Pro Cys Tyr Ala Glu Lys Asp Gly Ala Arg | |
| 1950 1955 1960 | |
| gta atg gct ggg aaa gtg gag atg aca ttg gaa atc ctc aac gag | 6013 |
| Val Met Ala Gly Lys Val Glu Met Thr Leu Glu Ile Leu Asn Glu | |
| 1965 1970 1975 | |
| aag gag gcc gac gag agg cca gcc ggg aag ggg cgg gac gaa ccc | 6058 |
| Lys Glu Ala Asp Glu Arg Pro Ala Gly Lys Gly Arg Asp Glu Pro | |
| 1980 1985 1990 | |
| aac atg aac ccc aag ctg gac tta cca aat cga cca gaa acc tcc | 6103 |
| Asn Met Asn Pro Lys Leu Asp Leu Pro Asn Arg Pro Glu Thr Ser | |
| 1995 2000 2005 | |
| ttc ctc tgg ttc acc aac cca tgc aag acc atg aag ttc atc gtg | 6148 |
| Phe Leu Trp Phe Thr Asn Pro Cys Lys Thr Met Lys Phe Ile Val | |
| 2010 2015 2020 | |
| tgg cgc cgc ttt aag tgg gtc atc atc ggc ttg ctg ttc ctg ctt | 6193 |
| Trp Arg Arg Phe Lys Trp Val Ile Ile Gly Leu Leu Phe Leu Leu | |
| 2025 2030 2035 | |
| atc ctg ctg ctc ttc gtg gcc gtg ctc ctc tac tct ttg ccg aac | 6238 |
| Ile Leu Leu Leu Phe Val Ala Val Leu Leu Tyr Ser Leu Pro Asn | |
| 2040 2045 2050 | |
| tat ttg tca atg aag att gta aag cca aat gtg taa caaaggcaaa | 6284 |
| Tyr Leu Ser Met Lys Ile Val Lys Pro Asn Val | |
| 2055 2060 | |
| ggcttcattt caagagtcac ccagcaatga gagaatcctg cctctgtaga ccaacatcca | 6344 |
| gtgtgatttt gtgtctgaga ccacacccca gtagcagggtt acgccatgtc accgagcccc | 6404 |
| attgattccc agagggtcct agtcctggaa agtcaggcca acaagcaacg tttgcatcat | 6464 |
| gttatctctt aagtattaaa agttttattt tctaaagttt aaatcatgtt tttcaaaata | 6524 |
| tttttcaagg tggctgggtc catttaaaaa tcatcttttt atatgtgtct tcggttctag | 6584 |
| acttcagctt ttggaaattg ctaaatagaa ttcaaaaaatc tctgcatcct gaggtgatat | 6644 |
| acttcatatt tgtaatcaac tgaaagagct gtgcattata aaatcagtta gaatagttag | 6704 |

aacaattctt atttatgccc acaaccattg ctatatatttg tatggatgtc ataaaagtct 6764
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Phe Gly Lys Pro Asp Pro Ile Val Ser Val Ile Phe Lys Asp Glu Lys
 20 25 30

Lys Lys Thr Lys Lys Val Asp Asn Glu Leu Asn Pro Val Trp Asn Glu
 35 40 45

Ile Leu Glu Phe Asp Leu Arg Gly Ile Pro Leu Asp Phe Ser Ser Ser
 50 55 60

Leu Gly Ile Ile Val Lys Asp Phe Glu Thr Ile Gly Gln Asn Lys Leu
 65 70 75 80

Ile Gly Thr Ala Thr Val Ala Leu Lys Asp Leu Thr Gly Asp Gln Ser
 85 90 95

Arg Ser Leu Pro Tyr Lys Leu Ile Ser Leu Leu Asn Glu Lys Gly Gln
 100 105 110

Asp Thr Gly Ala Thr Ile Asp Leu Val Ile Gly Tyr Asp Pro Pro Ser
 115 120 125

Ala Pro His Pro Asn Asp Leu Ser Gly Pro Ser Val Pro Gly Met Gly
 130 135 140

Gly Asp Gly Glu Glu Asp Glu Gly Asp Glu Asp Arg Leu Asp Asn Ala
 145 150 155 160

Val Arg Gly Pro Gly Pro Lys Gly Pro Val Gly Thr Val Ser Glu Ala
 165 170 175

Gln Leu Ala Arg Arg Leu Thr Lys Val Lys Asn Ser Arg Arg Met Leu
 180 185 190

Ser Asn Lys Pro Gln Asp Phe Gln Ile Arg Val Arg Val Ile Glu Gly
 195 200 205

Arg Gln Leu Ser Gly Asn Asn Ile Arg Pro Val Val Lys Val His Val
 210 215 220

Cys Gly Gln Thr His Arg Thr Arg Ile Lys Arg Gly Asn Asn Pro Phe
 225 230 235 240

Phe Asp Glu Leu Phe Phe Tyr Asn Val Asn Met Thr Pro Ser Glu Leu
 245 250 255

Met Asp Glu Ile Ile Ser Ile Arg Val Tyr Asn Ser His Ser Leu Arg
 260 265 270

Ala Asp Cys Leu Met Gly Glu Phe Lys Ile Asp Val Gly Phe Val Tyr
 275 280 285

Asp Glu Pro Gly His Ala Val Met Arg Lys Trp Leu Leu Leu Asn Asp
 290 295 300

Pro Glu Asp Thr Ser Ser Gly Ser Lys Gly Tyr Met Lys Val Ser Met
 305 310 315 320

Phe Val Leu Gly Thr Gly Asp Glu Pro Pro Pro Glu Arg Arg Asp Arg
 325 330 335

Asp Asn Asp Ser Asp Asp Val Glu Ser Asn Leu Leu Leu Pro Ala Gly
 340 345 350

Ile Ala Leu Arg Trp Val Thr Phe Leu Leu Lys Ile Tyr Arg Ala Glu
 355 360 365

Asp Ile Pro Gln Met Asp Asp Ala Phe Ser Gln Thr Val Lys Glu Ile
 370 375 380

Phe Gly Gly Asn Ala Asp Lys Lys Asn Leu Val Asp Pro Phe Val Glu

Val Ser Phe Ala Gly Lys Lys Val Cys Thr Asn Ile Ile Glu Lys Asn
 405 410 415

Ala Asn Pro Glu Trp Asn Gln Val Val Asn Leu Gln Ile Lys Phe Pro
 420 425 430

Ser Val Cys Glu Lys Ile Lys Leu Thr Ile Tyr Asp Trp Asp Arg Leu
 435 440 445

Thr Lys Asn Asp Val Val Gly Thr Thr Tyr Leu His Leu Ser Lys Ile
 450 455 460

Ala Ala Ser Gly Gly Glu Val Glu Asp Phe Ser Ser Ser Gly Thr Gly
 465 470 475 480

Ala Ala Ser Tyr Thr Val Asn Thr Gly Glu Thr Glu Val Gly Phe Val
 485 490 495

Pro Thr Phe Gly Pro Cys Tyr Leu Asn Leu Tyr Gly Ser Pro Arg Glu
 500 505 510

Tyr Thr Gly Phe Pro Asp Pro Tyr Asp Glu Leu Asn Thr Gly Lys Gly
 515 520 525

Glu Gly Val Ala Tyr Arg Gly Arg Ile Leu Val Glu Leu Ala Thr Phe
 530 535 540

Leu Glu Lys Thr Pro Pro Asp Lys Lys Leu Glu Pro Ile Ser Asn Asp
 545 550 555 560

Asp Leu Leu Val Val Glu Lys Tyr Gln Arg Arg Arg Lys Tyr Ser Leu
 565 570 575

Ser Ala Val Phe His Ser Ala Thr Met Leu Gln Asp Val Gly Glu Ala
 580 585 590

Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe Asp Thr
 595 600 605

Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala Val Phe
 610 615 620

Asp Gly Asn Tyr Tyr Tyr Tyr Leu Pro Trp Ala His Thr Lys Pro Val
 625 630 635 640

Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg Leu Asp Ala
 645 650 655

Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr Asn Ile Glu
 660 665 670

Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn Gln Leu Ala

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Pro | Glu | Arg | Ser | Leu | Leu | Thr | Glu | Ala | Asp | Ala | Gly | His | Thr |
| | | 915 | | | | | 920 | | | | | 925 | | | |

Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr Pro Gly Gly
 930 935 940

Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn Gly Asp Lys
 945 950 955 960

Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp Glu Trp Glu
 965 970 975

Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp Glu Lys Gly
 980 985 990

Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp
 995 1000 1005

Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu
 1010 1015 1020

Val Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser Thr
 1025 1030 1035

Ala Arg Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr
 1040 1045 1050

Ala Ser Leu Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser
 1055 1060 1065

Asp Thr Phe Arg Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser
 1070 1075 1080

Glu Thr His Gly Ala Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu
 1085 1090 1095

Gly Ala Asp Thr Thr Glu Asp Gly Asp Glu Lys Ser Leu Glu Lys
 1100 1105 1110

Gln Lys His Ser Ala Thr Thr Val Phe Gly Ala Asn Thr Pro Ile
 1115 1120 1125

Val Ser Cys Asn Phe Asp Arg Val Tyr Ile Tyr His Leu Arg Cys
 1130 1135 1140

Tyr Val Tyr Gln Ala Arg Asn Leu Leu Ala Leu Asp Lys Asp Ser
 1145 1150 1155

| | | | |
|---------|---------------------|---------------------|-------------|
| Phe Ser | Asp Pro Tyr Ala His | Ile Cys Phe Leu His | Arg Ser Lys |
| 1160 | 1165 | 1170 | |
| Thr Thr | Glu Ile Ile His Ser | Thr Leu Asn Pro Thr | Trp Asp Gln |
| 1175 | 1180 | 1185 | |
| Thr Ile | Ile Phe Asp Glu Val | Glu Ile Tyr Gly Glu | Pro Gln Thr |
| 1190 | 1195 | 1200 | |
| Val Leu | Gln Asn Pro Pro Lys | Val Ile Met Glu Leu | Phe Asp Asn |
| 1205 | 1210 | 1215 | |
| Asp Gln | Val Gly Lys Asp Glu | Phe Leu Gly Arg Ser | Ile Phe Ser |
| 1220 | 1225 | 1230 | |
| Pro Val | Val Lys Leu Asn Ser | Glu Met Asp Ile Thr | Pro Lys Leu |
| 1235 | 1240 | 1245 | |
| Leu Trp | His Pro Val Met Asn | Gly Asp Lys Ala Cys | Gly Asp Val |
| 1250 | 1255 | 1260 | |
| Leu Val | Thr Ala Glu Leu Ile | Leu Arg Gly Lys Asp | Gly Ser Asn |
| 1265 | 1270 | 1275 | |
| Leu Pro | Ile Leu Pro Pro Gln | Arg Ala Pro Asn Leu | Tyr Met Val |
| 1280 | 1285 | 1290 | |
| Pro Gln | Gly Ile Arg Pro Val | Val Gln Leu Thr Ala | Ile Glu Ile |
| 1295 | 1300 | 1305 | |
| Leu Ala | Trp Gly Leu Arg Asn | Met Lys Asn Phe Gln | Met Ala Ser |
| 1310 | 1315 | 1320 | |
| Ile Thr | Ser Pro Ser Leu Val | Val Glu Cys Gly Gly | Glu Arg Val |
| 1325 | 1330 | 1335 | |
| Glu Ser | Val Val Ile Lys Asn | Leu Lys Lys Thr Pro | Asn Phe Pro |
| 1340 | 1345 | 1350 | |
| Ser Ser | Val Leu Phe Met Lys | Val Phe Leu Pro Lys | Glu Glu Leu |
| 1355 | 1360 | 1365 | |
| Tyr Met | Pro Pro Leu Val Ile | Lys Val Ile Asp His | Arg Gln Phe |
| 1370 | 1375 | 1380 | |
| Gly Arg | Lys Pro Val Val Gly | Gln Cys Thr Ile Glu | Arg Leu Asp |

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| | | |
|-----------------|-----------------------------|-----------------------------|
| 1385 | 1390 | 1395 |
| Arg Phe 1400 | Arg Cys Asp Pro Tyr 1405 | Ala Gly Lys Glu Asp 1410 |
| Gln Leu 1415 | Lys Ala Ser Leu Leu 1420 | Ser Ala Pro Pro Cys 1425 |
| Val Ile 1430 | Glu Met Glu Asp Thr 1435 | Lys Pro Leu Leu Ala 1440 |
| Thr Glu 1445 | Lys Glu Glu Glu Ile 1450 | Val Asp Trp Trp Ser 1455 |
| Ala Ser 1460 | Ser Gly Glu His Glu 1465 | Lys Cys Gly Gln Tyr 1470 |
| Gly Tyr 1475 | Ser Lys Leu Lys Ile 1480 | Tyr Asn Cys Glu Leu 1485 |
| Ala Glu 1490 | Phe Glu Gly Leu Thr 1495 | Asp Phe Ser Asp Thr 1500 |
| Tyr Arg | Gly Lys Ser Asp Glu | Asn Glu Asp Pro Ser |
| Glu Phe 1520 | Lys Gly Ser Phe Arg 1525 | Ile Tyr Pro Leu Pro 1530 |
| Ser Val 1535 | Pro Ala Pro Pro Arg 1540 | Gln Phe Arg Glu Leu 1545 |
| Val Pro 1550 | Gln Glu Cys Thr Val 1555 | Arg Ile Tyr Ile Val 1560 |
| Glu Leu 1565 | Gln Pro Gln Asp Asn 1570 | Asn Gly Leu Cys Asp 1575 |
| Lys Ile 1580 | Thr Leu Gly Lys Lys 1585 | Val Ile Glu Asp Arg 1590 |
| Ile Pro 1595 | Asn Thr Leu Asn Pro 1600 | Val Phe Gly Arg Met 1605 |
| Ser Cys 1610 | Tyr Leu Pro Gln Glu 1615 | Lys Asp Leu Lys Ile 1620 |

Asp Tyr Asp Thr Phe Thr Arg Asp Glu Lys Val Gly Glu Thr Ile
 1625 1630 1635
 Ile Asp Leu Glu Asn Arg Phe Leu Ser Arg Phe Gly Ser His Cys
 1640 1645 1650
 Gly Ile Pro Glu Glu Tyr Cys Val Ser Gly Val Asn Thr Trp Arg
 1655 1660 1665
 Asp Gln Leu Arg Pro Thr Gln Leu Leu Gln Asn Val Ala Arg Phe
 1670 1675 1680
 Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu Asp Gly Ser Arg Ile
 1685 1690 1695
 Arg Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu Phe Glu Ala Asn
 1700 1705 1710
 Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu Arg Leu Ala
 1715 1720 1725
 Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His Val Glu
 1730 1735 1740
 Thr Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Gln Gly
 1745 1750 1755
 Lys Leu Gln Met Trp Val Asp Val Phe Pro Lys Ser Leu Gly Pro
 1760 1765 1770
 Pro Gly Pro Pro Phe Asn Ile Thr Pro Arg Lys Ala Lys Lys Tyr
 1775 1780 1785
 Tyr Leu Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp
 1790 1795 1800
 Glu Lys Ser Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys
 1805 1810 1815
 Gly Trp Ile Pro Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val
 1820 1825 1830
 His Tyr Arg Ser Leu Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe
 1835 1840 1845
 Val Phe Pro Phe Asp Tyr Leu Pro Ala Glu Gln Leu Cys Ile Val

| | | |
|-----------------------------|---------------------|-------------|
| 1850 | 1855 | 1860 |
| Ala Lys Lys Glu His Phe Trp | Ser Ile Asp Gln Thr | Glu Phe Arg |
| 1865 | 1870 | 1875 |
| Ile Pro Pro Arg Leu Ile Ile | Gln Ile Trp Asp Asn | Asp Lys Phe |
| 1880 | 1885 | 1890 |
| Ser Leu Asp Asp Tyr Leu Gly | Phe Leu Glu Leu Asp | Leu Arg His |
| 1895 | 1900 | 1905 |
| Thr Ile Ile Pro Ala Lys Ser | Pro Glu Lys Cys Arg | Leu Asp Met |
| 1910 | 1915 | 1920 |
| Ile Pro Asp Leu Lys Ala Met | Asn Pro Leu Lys Ala | Lys Thr Ala |
| 1925 | 1930 | 1935 |
| Ser Leu Phe Glu Gln Lys Ser | Met Lys Gly Trp Trp | Pro Cys Tyr |
| 1940 | 1945 | 1950 |
| Ala Glu Lys Asp Gly Ala Arg | Val Met Ala Gly Lys | Val Glu Met |
| 1955 | 1960 | 1965 |
| Thr Leu Glu Ile Leu Asn Glu | Lys Glu Ala Asp Glu | Arg Pro Ala |
| 1970 | 1975 | 1980 |
| Gly Lys Gly Arg Asp Glu Pro | Asn Met Asn Pro Lys | Leu Asp Leu |
| 1985 | 1990 | 1995 |
| Pro Asn Arg Pro Glu Thr Ser | Phe Leu Trp Phe Thr | Asn Pro Cys |
| 2000 | 2005 | 2010 |
| Lys Thr Met Lys Phe Ile Val | Trp Arg Arg Phe Lys | Trp Val Ile |
| 2015 | 2020 | 2025 |
| Ile Gly Leu Leu Phe Leu Leu | Ile Leu Leu Leu Phe | Val Ala Val |
| 2030 | 2035 | 2040 |
| Leu Leu Tyr Ser Leu Pro Asn | Tyr Leu Ser Met Lys | Ile Val Lys |
| 2045 | 2050 | 2055 |
| Pro Asn Val | | |
| 2060 | | |

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tgtaggtctg gcaagc

16

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18

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gggtctgacg ctcacg

16

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gataggtgcc tcactg

16

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19

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19

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<400> 241

ggaagtggat ggacatttt

19

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<223> RNAi molecule

<400> 242

ggucagagcu ggaggauuu

19

<210> 243

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<400> 243

gaaagaagga gacccguua

19

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<223> RNAi molecule

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ccaagaagau cuacaaugg

19

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<223> RNAi molecule

<400> 245

ggaacugcau gcugaauga

19

<210> 246

<211> 27

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<213> Artificial Sequence

<220>

<223> RNAi molecule

<400> 246

uagaccugcu cagccuucug gauacuu

27

<210> 247

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<212> RNA

<213> Artificial Sequence

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<223> RNAi molecule

<400> 247

cuucucauaa uugaaguggu ugucguu

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gugugucuuc ucauaauuga agugguu

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27

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<400> 251

ccucuugaga ucagguuggc agucauu

27

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PATENT COOPERATION TREATY

PCT/US03/037143

From the INTERNATIONAL BUREAU

PCTNOTIFICATION CONCERNING
SUBMISSION OR TRANSMITTAL
OF PRIORITY DOCUMENT

(PCT Administrative Instructions, Section 411)

To:

RYBAK, Sheree, Lynn
Klarquist Sparkman, LLP
Suite 1600
One World Trade Center
121 SW Salmon Street
Portland, OR 97204
ETATS-UNIS D'AMERIQUE

| | |
|--|---|
| Date of mailing (day/month/year) 29 September 2004 (29.09.2004) | |
| Applicant's or agent's file reference 6395-66741 | IMPORTANT NOTIFICATION |
| International application No. PCT/US03/037143 | International filing date (day/month/year) 18 November 2003 (18.11.2003) |
| International publication date (day/month/year) 19 August 2004 (19.08.2004) | Priority date (day/month/year) 18 November 2002 (18.11.2002) |
| Applicant THE GOVERNMENT OF THE UNITED STATES OF AMERICA as represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION et al | |

- By means of this Form, which replaces any previously issued notification concerning submission or transmittal of priority documents, the applicant is hereby notified of the date of receipt by the International Bureau of the priority document(s) relating to all earlier application(s) whose priority is claimed. Unless otherwise indicated by the letters "NR", in the right-hand column or by an asterisk appearing next to a date of receipt, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).
- (If applicable) The letters "NR" appearing in the right-hand column denote a priority document which, on the date of mailing of this Form, had not yet been received by the International Bureau under Rule 17.1(a) or (b). Where, under Rule 17.1(a), the priority document must be submitted by the applicant to the receiving Office or the International Bureau, but the applicant fails to submit the priority document within the applicable time limit under that Rule, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.
- (If applicable) An asterisk (*) appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b) (the priority document was received after the time limit prescribed in Rule 17.1(a) or the request to prepare and transmit the priority document was submitted to the receiving Office after the applicable time limit under Rule 17.1(b)). Even though the priority document was not furnished in compliance with Rule 17.1(a) or (b), the International Bureau will nevertheless transmit a copy of the document to the designated Offices, for their consideration. In case such a copy is not accepted by the designated Office as the priority document, Rule 17.1(c) provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

| Priority date | Priority application No. | Country or regional Office or PCT receiving Office | Date of receipt of priority document |
|-------------------------------|--------------------------|---|---|
| 18 November 2002 (18.11.2002) | 60/427,484 | US | 02 September 2004 (02.09.2004) |

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08.10.2004

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| The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland | Authorized officer Cruz Juan |
| Facsimile No. +41 22 740 14 35 | Facsimile No. +41 22 338 89 65 Telephone No. +41 22 338 8239 |

From the INTERNATIONAL BUREAU

PCTNOTIFICATION CONCERNING
SUBMISSION OR TRANSMITTAL
OF PRIORITY DOCUMENT

(PCT Administrative Instructions, Section 411)

To:

RYBAK, Sheree, Lynn
Klarquist Sparkman, LLP
Suite 1600
One World Trade Center
121 SW Salmon Street
Portland, OR 97204
ETATS-UNIS D'AMERIQUE

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| Date of mailing (day/month/year) 29 September 2004 (29.09.2004) | |
| Applicant's or agent's file reference 6395-66741 | IMPORTANT NOTIFICATION |
| International application No. PCT/US03/037143 | International filing date (day/month/year) 18 November 2003 (18.11.2003) |
| International publication date (day/month/year) 19 August 2004 (19.08.2004) | Priority date (day/month/year) 18 November 2002 (18.11.2002) |
| Applicant THE GOVERNMENT OF THE UNITED STATES OF AMERICA as represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION et al | |

- By means of this Form, which replaces any previously issued notification concerning submission or transmittal of priority documents, the applicant is hereby notified of the date of receipt by the International Bureau of the priority document(s) relating to all earlier application(s) whose priority is claimed. Unless otherwise indicated by the letters "NR", in the right-hand column or by an asterisk appearing next to a date of receipt, the priority document concerned was submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b).
- (If applicable) The letters "NR" appearing in the right-hand column denote a priority document which, on the date of mailing of this Form, had not yet been received by the International Bureau under Rule 17.1(a) or (b). Where, under Rule 17.1(a), the priority document must be submitted by the applicant to the receiving Office or the International Bureau, but the applicant fails to submit the priority document within the applicable time limit under that Rule, the attention of the applicant is directed to Rule 17.1(c) which provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.
- (If applicable) An asterisk (*) appearing next to a date of receipt, in the right-hand column, denotes a priority document submitted or transmitted to the International Bureau but not in compliance with Rule 17.1(a) or (b) (the priority document was received after the time limit prescribed in Rule 17.1(a) or the request to prepare and transmit the priority document was submitted to the receiving Office after the applicable time limit under Rule 17.1(b)). Even though the priority document was not furnished in compliance with Rule 17.1(a) or (b), the International Bureau will nevertheless transmit a copy of the document to the designated Offices, for their consideration. In case such a copy is not accepted by the designated Office as the priority document, Rule 17.1(c) provides that no designated Office may disregard the priority claim concerned before giving the applicant an opportunity, upon entry into the national phase, to furnish the priority document within a time limit which is reasonable under the circumstances.

| Priority date | Priority application No. | Country or regional Office or PCT receiving Office | Date of receipt of priority document |
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| 18 November 2002 (18.11.2002) | 60/427,464 | US | 02 September 2004 (02.09.2004) |
| 25 June 2003 (25.06.2003) | 60/482,604 | US | 02 September 2004 (02.09.2004) |

EPO - DO 1

08. 10. 2004

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|---|---|
| The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland | Authorized officer Higuera Luis |
| Facsimile No. +41 22 740 14 35 | Facsimile No. +41 22 338 89 65 Telephone No. +41 22 338 8154 |



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2280 HV Rijswijk (ZH)
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Europäisches
Patentamt

Eingangs-
stelle

European
Patent Office

Receiving
Section

Office européen
des brevets

Section de
Dépôt

WIPO
The International Bureau
34, Chemin des Colombettes
CH-1211 GENEVA 20
SWITZERLAND

REC'D 07 JUL 2005

WIPO

PCT

Datum/Date

06-07-2005

Zeichen/Ref./Réf.

FB15612/E19923E

Anmeldung Nr./Application No./Demande n°/Patent Nr./Patent No./Brevet n°.

PCT/US0337143 - EP/03815298.9-1212 / ISA US

Anmelder/Applicant/Demandeur/Patentinhaber/Proprietor/Titulaire

The Government of the United States of America, as represented by the Secretary,, et al

For the aforementioned international application, you are hereby kindly
requested to forward to the EPO in its capacity as designated/elected
Office:

- ☒ a) the publication of the international search report. (Art. 20 PCT)
- ☐ b) the copy of the international preliminary examination report
(Art. 36(3)(a) PCT)
- ☐ c) the copy (copies) of the priority document(s). If any document is
not available and ISA is not EP, please indicate below whether
the receiving Office has been requested to transmit the document
to the International Bureau (Form PCT/RO/101, Box VI;
Rule 17.1(b) PCT).
- ☐

RECEIVING SECTION

Answer of the International Bureau [IB]:

- ☐ The requested item [a), b) or c)] is not available with the IB.

Reason:

For priority documents [c)] with ISA not EP:

- ☐ The applicant has requested the receiving Office to issue a priority
document (Rule 17.1(b) PCT) but the IB has not received it.

The International Bureau

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15. 07. 2005

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communication des documents du PCT

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☐ ISR waiting for publication

☐ ISR will be published on

☒ ISR not received, ISA / US

☐ P. Doc. not received

☐ Has been requested pursuant to Rule 17.1(b) PCT

☐ Has not been requested pursuant to Rule 17.1(b) PCT

☐ IPER not available, IPEA

☐ IPER translation not yet available

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15. 07. 2005

TEAM 14



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2250 HV Rixswijk (ZH)
☎ (070) 3 40 20 40
FAX (070) 3 40 30 16

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Portland, OR 97204
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EPO Customer Services

Tel.: +31 (0)70 340 45 00

Date

24.06.05

| | |
|---|---|
| Reference | Application No./Patent No. 03815298.9 - 2405 PCT/US0337143 |
| Applicant/Proprietor The Government of the United States of America, as represented by the Secretary, Department of Health & Human Services, et al | |

Entry into the European phase before the European Patent Office

These notes describe the procedural steps required for entry into the European phase before the European Patent Office (EPO). You are advised to read them carefully: failure to take the necessary action in time can lead to your application being deemed withdrawn.

1. The above-mentioned international patent application has been given European application No. 03815298.9.
2. Applicants without a residence or their principal place of business in an EPC contracting state may themselves initiate European processing of their international applications, provided they do so before expiry of the 31st month from the priority date (see also point 6 below).

During the European phase before the EPO as designated or elected Office, however, such applicants must be represented by a professional representative (Arts. 133(2) and 134(1), (7) EPC).

Procedural acts performed after expiry of the 31st month by a professional representative who acted during the international phase but is not authorised to act before the EPO have no legal effect and therefore lead to loss of rights.

Please note that a professional representative authorised to act before the EPO and who acted for the applicant during the international phase does not automatically become the representative for the European phase. Applicants are therefore strongly advised to appoint in good time any representative they wish to initiate the European phase for them; otherwise, the EPO has to send all communications direct to the applicant.

3. Applicants with a residence or their principal place of business in an EPC contracting state are not obliged to appoint, for the European phase before the EPO as designated or elected Office, a professional representative authorised to act before the EPO.
However, in view of the complexity of the procedure it is recommended that they do so.
4. Applicants and professional representatives are also strongly advised to initiate the European phase using EPO Form 1200 (available free of charge from the EPO). This however is not compulsory.



5. To enter the European phase before the EPO, the following acts must be performed.
(N.B.: Failure validly to do so will entail loss of rights or other adverse legal consequences.)

5.1 If the EPO is acting as **designated** or **elected** Office (Arts. 22(1)(3) and 39(1) PCT respectively), applicants must, within 31 months from the date of filing or (where applicable) the earliest priority date:

a) Supply a translation of the international application into an EPO official language, if the International Bureau did not publish the application in such a language (Art. 22(1) PCT and Rule 107(1)(a) EPC).

If the translation is not filed in time, the international application is deemed withdrawn before the EPO (Rule 108(1) EPC).

This loss of rights is deemed not to have occurred if the translation is then filed within a two-month grace period as from notification of an EPO communication, provided a surcharge is paid at the same time (Rule 108(3) EPC).

b) Pay the national basic fee (EUR 160,00) and, where a supplementary European search report has to be drawn up, the search fee (EUR 690,00 ; Rule 107(1)(c) and (e) EPC).

c) If the time limit under Article 79(2) EPC expires before the 31-month time limit, pay the designation fee (EUR 75,00) for each contracting state designated (Rule 107(1)(d) EPC).

d) If the time limit under Article 94(2) EPC expires before the 31-month time limit, file the written request for examination and pay the examination fee (EUR 1430,00 ; Rule 107(1)(f) EPC).

e) Pay the third-year renewal fee (EUR 380,00) if it falls due before expiry of the 31-month time limit (Rule 107(1)(g) EPC).

If the fees under (b) to (d) above are not paid in time, or the written request for examination is not filed in time, the international application is deemed withdrawn before the EPO, or the contracting-state designation(s) in question is (are) deemed withdrawn (Rule 108(1) and (2) EPC). However, the fees may still be validly paid within a two-month grace period as from notification of an EPO communication, provided the necessary surcharges are paid at the same time (Rule 108(3) EPC). For the renewal fee under (e) above, the grace period is six months from the fee's due date (Article 86(2) EPC).

5.2 If the application documents on which the European grant procedure is to be based comprise more than ten claims, a claims fee is payable within the 31-month time limit under Rule 107(1) EPC for the eleventh and each subsequent claim (Rule 110(1) EPC). The fee can however still be paid within a one-month grace period as from notification of an EPO communication pointing out the failure to pay (Rule 110(2) EPC).

6. If the applicant had a representative during the application's international phase, the present notes will be sent to the representative, asking him to inform the applicant accordingly.

All subsequent communications will be sent to the applicant, or - if the EPO is informed of his appointment in time - to the applicant's European representative.



Date

Sheet 3

Application No. 03815298.9

7. For more details about time limits and procedural acts before the EPO as designated and elected Office, see the EPO brochure

How to get a European patent
Guide for applicants - Part 2
PCT procedure before the EPO - "Euro-PCT"

This brochure, the list of professional representatives before the EPO, Form 1200 and details of the latest fees are now all available on the Internet under

<http://www.european-patent-office.org>

RECEIVING SECTION





P.B. 5818 - Patentlaan 2
2280 HV Rijswijk (ZH)
☎ +31 70 340 2040
TX 31651 epo nl
FAX +31 70 340 3016

Europäisches
Patentamt
Eingangsstelle

European
Patent Office
Receiving
Section

Office européen
des brevets
Section de
Dépôt

WIPO
The International Bureau
34, Chemin des Colombettes
CH-1211 GENEVA 20
SWITZERLAND

Datum/Date

06-07-2005

Zeichen/Ref./Réf.

FB15612/E19923E

Anmeldung Nr./Application No./Demande n°/Patent Nr./Patent No./Brevet n°

PCT/US0337143 - EP/03815298.9-1212 / ISA US

Anmelder/Applicant/Demandeur/Patentinhaber/Proprietor/Titulaire

The Government of the United States of America, as represented by the Secretary,, et al

For the aforementioned international application, you are hereby kindly requested to forward to the EPO in its capacity as designated/elected Office:

- ☒ a) the publication of the international search report (Art. 20 PCT)
- ☐ b) the copy of the international preliminary examination report (Art. 36(3)(a) PCT)
- ☐ c) the copy (copies) of the priority document(s). If any document is not available and ISA is not EP, please indicate below whether the receiving Office has been requested to transmit the document to the International Bureau (Form PCT/RO/101, Box VI; Rule 17.1(b) PCT).
- ☐

RECEIVING SECTION

Answer of the International Bureau [IB]:

- ☐ The requested item [a), b) or c)] is not available with the IB.

Reason:

For priority documents [c)] with ISA not EP:

- ☐ The applicant has requested the receiving Office to issue a priority document (Rule 17.1(b) PCT) but the IB has not received it.

The International Bureau



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Europäisches
Patentamt

Eingangs-
stelle

European
Patent Office

Receiving
Section

Office européen
des brevets

Section de
Dépôt

WIPO
The International Bureau
34, Chemin des Colombettes
CH-1211 GENEVA 20
SWITZERLAND

Datum/Date

25-10-2005

Zeichen/Ref./Réf.

FB15612/E19923E

Anmeldung Nr./Application No./Demande n°./Patent Nr./Patent No./Brevet n°.

PCT/US0337143 - EP/03815298.9-1212 / ISA US

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☒ Pamphlet A3 still missing

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Durand-Fleith, Odette

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The International Bureau



P.B.5818 - Patentaan 2
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FAX (070) 3 40 30 16

**Europäisches
Patentamt**

**European
Patent Office**

**Office européen
des brevets**

Generaldirektion 1

Directorate General 1

Direction générale 1

Gowshall, Jonathan Vallance
FORRESTER & BOEHMERT
Pettenkoferstrasse 20-22
80336 München
ALLEMAGNE



EPO Customer Services

Tel.: +31 (0)70 340 45 00

Date

30.11.05

| | |
|--|---|
| Reference FB15612/E19923E | Application No./Patent No. 03815298.9 - 2405 PCT/US0337143 |
| Applicant/Proprietor The Government of the United States of America, asrepresented by the Secretary, Department of Health& Human Services, et al | |

Notification of European publication number and information on the application of Article 67(3) EPC

The provisional protection under Article 67(1) and (2) EPC in the individual contracting states becomes effective only when the conditions referred to in Article 67(3) EPC have been fulfilled (for further details, see information brochure of the European Patent Office "National Law relating to the EPC" and additional information in the Official Journal of the European Patent Office).

Pursuant to Article 158(1) EPC the publication under Article 21 PCT of an international application for which the European Patent Office is a designated Office takes the place of the publication of a European patent application.

The bibliographic data of the above-mentioned Euro-PCT application will be published on 11.01.06 in Section I.1 of the European Patent Bulletin. The European publication number is 1613724.

In all future communications to the European Patent Office, please quote the application number plus Directorate number.

Receiving Section





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Receiving
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des brevets

Section de
Dépôt

WIPO
The International Bureau
34, Chemin des Colombettes
CH-1211 GENEVA 20
SWITZERLAND

Datum/Date

07-06-2006

Zeichen/Ref./Réf.

FB15612/E19923E

Anmeldung Nr./Application No./Demande n°. /Patent Nr./Patent No./Brevet n°.

PCT/US0337143 - EP/03815298.9-1212 / ISA US

Anmelder/Applicant/Demandeur/Patentinhaber/Proprietor/Titulaire

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- ☒ b) the copy of the international preliminary examination report (Art. 36(3)(a) PCT)
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☐

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Reason:

For priority documents [c)] with ISA not EP:

☐ The applicant has requested the receiving Office to issue a priority document (Rule 17.1(b) PCT) but the IB has not received it.

The International Bureau

PATENT COOPERATION TREATY

PCT/US2003/037143

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

To:

European Patent Office
Phoenix Support Help Desk
Att. C. Hamm, Room S00G12, P.O. Box 5818
NL- 2280 HV Rijswijk
PAYS-BAS

in its capacity as elected Office

| | |
|--|--|
| Date of mailing (<i>day/month/year</i>) 03 November 2005 (03.11.2005) | |
| International application No. PCT/US2003/037143 | Applicant's or agent's file reference 6395-66741 |
| International filing date (<i>day/month/year</i>) 18 November 2003 (18.11.2003) | Priority date (<i>day/month/year</i>) 18 November 2002 (18.11.2002) |
| Applicant THE GOVERNMENT OF THE UNITED STATES OF AMERICA as represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION et al | |

1. The designated Office is hereby notified of its election made:



in the demand filed with the International Preliminary Examining Authority on:

07 June 2004 (07.06.2004)



in a notice effecting later election filed with the International Bureau on:

2. The election



was



was not

made before the expiration of 19 months from the priority date.

| | |
|---|--|
| The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland | Authorized officer Nora Lindner |
| Facsimile No.+41 22 740 14 35 | Facsimile No.+41 22 338 89 65 |

An das Europäische Patentamt

To the European Patent Office

A l'Office européen des brevets
EPO - Munich
85

20. Juni 2005

Eintritt in die
europäische Phase
(EPA als Bestimmungsamt
oder ausgewähltes Amt)Entry into the
European phase
(EPO as designated or
elected Office)Entrée dans la
phase européenne
(l'OEB agissant en qualité
d'office désigné ou élu)

| | | |
|--|---|--|
| Europäische Anmeldenummer oder, falls nicht bekannt, PCT-Aktenzeichen oder PCT-Veröffentlichungsnummer | European application number, or, if not known, PCT application or publication number PCT/US2003/037143 | Numéro de dépôt de la demande de brevet européen ou, à défaut, numéro de dépôt PCT ou de publication PCT |
| Zeichen des Anmelders oder Vertreters (max. 15 Positionen) | Applicant's or representative's reference (max. 15 spaces) FB15612 / E19923EP | Référence du demandeur ou du mandataire (15 caractères ou espaces au maximum) |
| <input checked="" type="checkbox"/> 1. Anmelder Die Angaben über den (die) Anmelder sind in der internationalen Veröffentlichung enthalten oder vom Internationalen Büro nach der internationalen Veröffentlichung vermerkt worden. <input type="checkbox"/> Änderungen, die das Internationale Büro noch nicht vermerkt hat, sind auf einem Zusatzblatt angegeben. Zustellanschrift (siehe Merkblatt II, 1) | 1. Applicant Indications concerning the applicant(s) are contained in the international publication or recorded by the International Bureau after the international publication. Changes which have not yet been recorded by the International Bureau are set out on an additional sheet. Address for correspondence (see Notes II, 1) | 1. Demandeur Les indications concernant le(s) demandeur(s) figurent dans la publication internationale ou ont été enregistrées par le Bureau international après la publication internationale. Les changements qui n'ont pas encore été enregistrés par le Bureau international sont indiqués sur une feuille additionnelle. Adresse pour la correspondance (voir notice II, 1) |
| 2. Vertreter Name (Nur einen Vertreter angeben, der in das europäische Patentregister eingetragen und an den zugestellt wird) Geschäftsanschrift Telefon Telefax Telex <input type="checkbox"/> Weitere(r) Vertreter auf Zusatzblatt | 2. Representative Name (Name only one representative who will be listed in the Register of European Patents and to whom notification will be made) GOWSHALL JON Address of place of business Forrester & Boehmert Pettenkoferstrasse 20-22 D-80336 München Telephone (+49) 89 55 96 80 Fax Telex (+49) 89 34 70 10 Additional representative(s) on additional sheet | 2. Mandataire Nom (N'indiquer qu'un seul mandataire, qui sera inscrit au Registre européen des brevets et auquel signification sera faite) Adresse professionnelle Téléphone (+3) 6 2707 Téléfax Télex Autre(s) mandataire(s) sur une feuille additionnelle |
| 3. Vollmacht <input type="checkbox"/> Einzelvollmacht ist beigelegt. <input type="checkbox"/> Allgemeine Vollmacht ist registriert unter Nummer: <input type="checkbox"/> Allgemeine Vollmacht ist eingereicht, aber noch nicht registriert. <input type="checkbox"/> Die beim EPA als PCT-Anmeldeamt eingereichte Vollmacht schließt ausdrücklich die europäische Phase ein. | 3. Authorisation Individual authorisation is attached. General authorisation has been registered under No: A general authorisation has been filed, but not yet registered. The authorisation filed with the EPO as PCT receiving Office expressly includes the European phase. | 3. Pouvoir Un pouvoir spécial est joint. Un pouvoir général a été enregistré sous le n° : Un pouvoir général a été déposé, mais n'est pas encore enregistré. Le pouvoir général déposé à l'OEB agissant en qualité d'office récepteur au titre du PCT s'applique expressément à la phase européenne. |

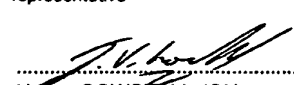
| | | |
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| <p><input checked="" type="checkbox"/> 4. Prüfungsantrag Hiermit wird die Prüfung der Anmeldung gemäß Art. 94 EPU beantragt. Die Prüfungsgebühr wird (wurde) entrichtet.</p> <p>Prüfungsantrag in einer zugelassenen Nichtamtssprache (siehe Merkblatt III, 5.2) :</p> | <p>4. Request for examination Examination of the application under Art. 94 EPC is hereby requested. The examination fee is being (has been, will be) paid.</p> <p>Request for examination in an admissible non-EPO language (see Notes III, 5.2) :</p> | <p>4. Requête en examen Il est demandé que soit examinée la demande de brevet conformément à l'art. 94 CBE. Il est (a été, sera) procédé au paiement de la taxe d'examen.</p> <p>Requête en examen dans une langue non officielle autorisée (voir notice III, 5.2) :</p> |
| <p><input checked="" type="checkbox"/> 5. Abschriften Zusätzliche Abschrift(en) der im ergänzenden europäischen Recherchenbericht angeführten Schriftstücke wird (werden) beantragt.</p> <p>Anzahl der zusätzlichen Sätze von Abschriften</p> | <p>5. Copies Additional copy (copies) of the documents cited in the supplementary European search report is (are) requested.</p> <p>Number of additional sets of copies</p> <p>2 (two)</p> | <p>5. Copies Prière de fournir une ou plusieurs copies supplémentaires des documents cités dans le rapport complémentaire de recherche européenne.</p> <p>Nombre de jeux supplémentaires de copies</p> |
| <p>6. Für das Verfahren vor dem EPA bestimmte Unterlagen</p> <p>6.1 Dem Verfahren vor dem EPA als Bestimmungsamt (PCT I) sind folgende Unterlagen zugrunde zu legen:</p> <p><input checked="" type="checkbox"/> die vom Internationalen Büro veröffentlichten Anmeldungsunterlagen (mit allen Ansprüchen, Beschreibung und Zeichnungen), gegebenenfalls mit den geänderten Ansprüchen nach Art. 19 PCT</p> <p><input type="checkbox"/> soweit sie nicht ersetzt werden durch die beigefügten Änderungen.</p> <p><i>Falls nötig, sind Klarstellungen auf einem Zusatzblatt einzureichen!</i></p> <p>6.2 Dem Verfahren vor dem EPA als ausgewähltem Amt (PCT II) sind folgende Unterlagen zugrunde zu legen:</p> <p><input checked="" type="checkbox"/> die dem Internationalen vorläufigen Prüfungsbericht zugrunde gelegten Unterlagen, einschließlich seiner eventuellen Anlagen (Solche Anlagen müssen immer beigefügt werden)</p> <p><input type="checkbox"/> soweit sie nicht ersetzt werden durch die beigefügten Änderungen.</p> <p><i>Falls nötig, sind Klarstellungen auf einem Zusatzblatt einzureichen!</i></p> <p><input checked="" type="checkbox"/> Sind dem EPA als mit der internationalen vorläufigen Prüfung beauftragten Behörde Versuchsberichte zugegangen, dürfen diese dem Verfahren vor dem EPA zugrunde gelegt werden.</p> | <p>6. Documents intended for proceedings before the EPO</p> <p>6.1 Proceedings before the EPO as designated Office (PCT I) are to be based on the following documents:</p> <p>the application documents published by the International Bureau (with all claims, description and drawings), where applicable with amended claims under Art. 19 PCT</p> <p>unless replaced by the amendments enclosed.</p> <p><i>Where necessary, clarifications must be submitted on a separate sheet!</i></p> <p>6.2 Proceedings before the EPO as elected Office (PCT II) are to be based on the following documents:</p> <p>the documents on which the international preliminary examination report is based, including its possible annexes (Such annexes must always be filed)</p> <p>unless replaced by the amendments enclosed.</p> <p><i>Where necessary, clarifications must be submitted on a separate sheet!</i></p> <p>If the EPO as International Preliminary Examining Authority has received test reports, these may be used as the basis of proceedings before the EPO.</p> | <p>6. Pièces destinées à la procédure devant l'OEB</p> <p>6.1 La procédure devant l'OEB agissant en qualité d'office désigné (PCT I) doit se fonder sur les pièces suivantes :</p> <p>les pièces de la demande publiée par le Bureau international (avec toutes les revendications, la description et les dessins), éventuellement avec les revendications modifiées conformément à l'article 19 du PCT</p> <p>dans la mesure où elles ne sont pas remplacées par les modifications jointes.</p> <p><i>Le cas échéant, des explications doivent être jointes sur une feuille additionnelle!</i></p> <p>6.2 La procédure devant l'OEB agissant en qualité d'office élu (PCT II) doit se fonder sur les pièces suivantes :</p> <p>les pièces sur lesquelles se fonde le rapport d'examen préliminaire international, y compris ses annexes éventuelles (De telles annexes sont toujours à joindre)</p> <p>dans la mesure où elles ne sont pas remplacées par les modifications jointes.</p> <p><i>Le cas échéant, des explications doivent être jointes sur une feuille additionnelle!</i></p> <p>Si l'OEB, agissant en qualité d'administration chargée de l'examen préliminaire international, a reçu des rapports d'essais, ceux-ci peuvent constituer la base de la procédure devant l'OEB.</p> |

| | | |
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| <p>7. Übersetzungen Beigefügt sind die nachfolgend angekreuzten Übersetzungen in einer der Amtssprachen des EPA (Deutsch, Englisch, Französisch):</p> <ul style="list-style-type: none"> <input type="checkbox"/> Im Verfahren vor dem EPA als Bestimmungsamt oder ausgewähltem Amt (PCT I + II): <p><input type="checkbox"/> Übersetzung der ursprünglich eingereichten internationalen Anmeldung (Beschreibung, Ansprüche, etwaige Textbestandteile in den Zeichnungen), der veröffentlichten Zusammenfassung, und etwaiger Angaben über biologisches Material nach Regel 13^{ter}.3 und 13^{ter}.4 PCT</p> <p><input type="checkbox"/> Übersetzung der prioritätsbegründenden Anmeldung(en)</p> <p><input type="checkbox"/> Es wird hiermit erklärt, daß die internationale Anmeldung in ihrer ursprünglich eingereichten Fassung eine vollständige Übersetzung der früheren Anmeldung ist (Regel 38(5) EPÜ)</p> <ul style="list-style-type: none"> <input type="checkbox"/> Zusätzlich im Verfahren vor dem EPA als Bestimmungsamt (PCT I): <p><input type="checkbox"/> Übersetzung der nach Art. 19 PCT geänderten Ansprüche nebst Erklärung, falls diese dem Verfahren vor dem EPA zugrunde gelegt werden sollen (siehe Feld 6)</p> <ul style="list-style-type: none"> <input type="checkbox"/> Zusätzlich im Verfahren vor dem EPA als ausgewähltem Amt (PCT II): <p><input type="checkbox"/> Übersetzung der Anlagen zum internationalen vorläufigen Prüfungsbericht</p> | <p>7. Translations Translations in one of the official languages of the EPO (English, French, German) are enclosed as crossed below:</p> <ul style="list-style-type: none"> <input type="checkbox"/> In proceedings before the EPO as designated or elected Office (PCT I + II): <p>Translation of the international application (description, claims, any text in the drawings) as originally filed, of the abstract as published and of any indication under Rule 13^{ter}.3 and 13^{ter}.4 PCT regarding biological material</p> <p>Translation of the priority application(s)</p> <p>It is hereby declared that the international application as originally filed is a complete translation of the previous application (Rule 38(5) EPC)</p> <ul style="list-style-type: none"> <input type="checkbox"/> In addition, in proceedings before the EPO as designated Office (PCT I): <p>Translation of amended claims and any statement under Art. 19 PCT, if the claims as amended are to form the basis for the proceedings before the EPO (see Section 6)</p> <ul style="list-style-type: none"> <input type="checkbox"/> In addition, in proceedings before the EPO as elected Office (PCT II): <p>Translation of any annexes to the international preliminary examination report</p> | <p>7. Traductions Vous trouverez, ci-joint, les traductions cochées ci-après dans l'une des langues officielles de l'OEB (allemand, anglais, français) :</p> <ul style="list-style-type: none"> <input type="checkbox"/> Dans la procédure devant l'OEB agissant en qualité d'office désigné ou élu (PCT I + II): <p>Traduction de la demande internationale telle que déposée initialement (description, revendications, textes figurant éventuellement dans les dessins), de l'abrégé publié, et de toutes indications visées aux règles 13^{ter}.3 et 13^{ter}.4 du PCT concernant le matériel biologique</p> <p>Traduction de la (des) demande(s) ouvrant le droit de priorité</p> <p>Il est déclaré par la présente que la demande internationale telle que déposée initialement est une traduction intégrale de la demande antérieure (règle 38(5) CBE)</p> <ul style="list-style-type: none"> <input type="checkbox"/> De plus, dans la procédure devant l'OEB agissant en qualité d'office désigné (PCT I) : <p>Traduction des revendications modifiées et de la déclaration faite conformément à l'article 19 du PCT, si la procédure devant l'OEB doit être fondée sur les revendications modifiées (voir la rubrique 6)</p> <ul style="list-style-type: none"> <input type="checkbox"/> De plus, dans la procédure devant l'OEB agissant en qualité d'office élu (PCT II) : <p>Traduction des annexes du rapport d'examen préliminaire international</p> |
| <p><input type="checkbox"/> 8. Biologisches Material Die Erfindung bezieht sich auf bzw. verwendet biologisches Material, das nach Regel 28 EPÜ hinterlegt worden ist.</p> <p><input type="checkbox"/> Die Angaben nach Regel 28(1)c) EPÜ (falls noch nicht bekannt, die Hinterlegungsstelle und das (die) Bezugszeichen (Nummer, Symbole usw.) des Hinterlegers) sind in der internationalen Veröffentlichung oder in der gemäß Feld 7 eingereichten Übersetzung enthalten auf:</p> <p>Seite(n) / Zeile(n)</p> <p><input type="checkbox"/> Die Empfangsbescheinigung(en) der Hinterlegungsstelle</p> <p><input type="checkbox"/> ist (sind) beigelegt</p> <p><input type="checkbox"/> wird (werden) nachgereicht</p> <p><input type="checkbox"/> Verzicht auf die Verpflichtung des Antragstellers nach Regel 28(3) EPÜ auf gesondertem Schriftstück</p> | <p>8. Biological material The invention relates to and/or uses biological material deposited under Rule 28 EPC.</p> <p>The particulars referred to in Rule 28(1)c) EPC (if not yet known, the depository institution and the identification reference(s) (number, symbols etc.) of the depositor) are given in the international publication or in the translation submitted under Section 7 on:</p> <p>page(s) / line(s)</p> <p>The receipt(s) of deposit issued by the depository institution</p> <p>is (are) enclosed</p> <p>will be filed at a later date</p> <p>Waiver of the right to an undertaking from the requester pursuant to Rule 28(3) EPC attached.</p> | <p>8. Matière biologique L'invention concerne et/ou utilise de la matière biologique, déposée conformément à la règle 28 CBE.</p> <p>Les indications visées à la règle 28(1)c) CBE (si non encore connues, l'autorité de dépôt et la (les) référence(s) d'identification (numéro ou symboles etc.) du déposant) figurent dans la publication internationale ou dans une traduction produite conformément à la rubrique 7 à la / aux:</p> <p>page(s) / lignes)</p> <p>Le(s) récépissé(s) de dépôt délivré(s) par l'autorité de dépôt</p> <p>est (sont) joint(s)</p> <p>sera (seront) produit(s) ultérieurement</p> <p>Renonciation, sur document distinct, à l'engagement du requérant au titre de la règle 28(3) CBE.</p> |

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| <p>9. Nucleotid- und Aminosäuresequenzen <input type="checkbox"/> Die nach Regeln 5.2 und 13^{ter} PCT sowie Regel 111(3) EPÜ erforderlichen Unterlagen liegen dem EPA bereits vor.</p> <p><input type="checkbox"/> Das schriftliche Sequenzprotokoll wird anliegend nachgereicht.</p> <p><input type="checkbox"/> Das Sequenzprotokoll geht nicht über den Inhalt der Anmeldung in der ursprünglich eingereichten Fassung hinaus.</p> <p><input type="checkbox"/> Der vorgeschriebene Datenträger ist beigelegt.</p> <p><input type="checkbox"/> Die auf dem Datenträger gespeicherte Information stimmt mit dem schriftlichen Sequenzprotokoll überein.</p> | <p>9. Nucleotide and amino acid sequences The items necessary in accordance with Rules 5.2 and 13^{ter} PCT and Rule 111(3) EPC have already been furnished to the EPO.</p> <p>The written sequence listing is furnished herewith.</p> <p>The sequence listing does not include matter which goes beyond the content of the application as filed.</p> <p>The prescribed data carrier is enclosed.</p> <p>The information recorded on the data carrier is identical to the written sequence listing.</p> | <p>9. Séquences de nucléotides et d'acides aminés Les pièces requises selon les règles 5.2 et 13^{ter} PCT et la règle 111(3) CBE ont déjà été déposées auprès de l'OEB.</p> <p>La liste de séquences écrite est produite ci-joint.</p> <p>La liste de séquences ne contient pas d'éléments s'étendant au-delà du contenu de la demande telle qu'elle a été déposée.</p> <p>Le support de données prescrit est joint.</p> <p>L'information figurant sur le support de données est identique à celle que contient la liste de séquences écrite.</p> |
| <p>10. Benennungsgebühren</p> <p><input checked="" type="checkbox"/> 10.1 Es ist derzeit beabsichtigt, den siebenfachen Betrag einer Benennungsgebühr zu entrichten. Damit gelten die Benennungsgebühren für alle Vertragsstaaten des EPÜ¹ als entrichtet (Art. 2 Nr. 3 GebO), soweit sie in der internationalen Anmeldung bestimmt sind².</p> <p><input type="checkbox"/> 10.2 Abweichend von der Erklärung in Nr. 10.1 ist derzeit beabsichtigt, weniger als sieben Benennungsgebühren für folgende in der internationalen Anmeldung bestimmte Vertragsstaaten des EPÜ² zu entrichten:</p> <p>(1) <input type="text"/></p> <p>(2) <input type="text"/></p> <p>(3) <input type="text"/></p> <p>Soweit unter Nr. 10.2 Vertragsstaaten aufgeführt sind, wird beantragt, für die dort nicht aufgeführten Vertragsstaaten von der Zustellung einer Mitteilung nach Regel 108(3) EPÜ abzusehen.</p> <p><input checked="" type="checkbox"/> 10.3 Wird ein automatischer Abbuchungsauftrag erteilt (Feld 12), so wird das EPA beauftragt, bei Ablauf der Grundfrist nach Regel 107 (1)(d) EPÜ den siebenfachen Betrag einer Benennungsgebühr abzubuchen. Ist eine Erklärung nach Nr. 10.2 abgegeben worden, so sollen die Benennungsgebühren nur für die dort angegebenen Vertragsstaaten abgebucht werden, sofern dem EPA nicht bis zum Ablauf der Grundfrist ein anderslautender Auftrag zugeht.</p> | <p>10. Designation fees</p> <p>10.1 It is currently intended to pay seven times the amount of the designation fee. The designation fees for all the EPC contracting states¹ designated in the international application² are thereby deemed to have been paid (Art. 2 No. 3 RFees).</p> <p>10.2 The declaration in No. 10.1 does not apply. Instead, it is currently intended to pay fewer than seven designation fees for the following EPC contracting states² designated in the international application:</p> <p>(4) <input type="text"/></p> <p>(5) <input type="text"/></p> <p>(6) <input type="text"/></p> <p>If contracting states are indicated under No. 10.2, it is requested that no communication under Rule 108(3) EPC be issued for contracting states not thus indicated.</p> <p>10.3 If an automatic debit order has been issued (Section 12), the EPO is authorised, on expiry of the basic period under Rule 107(1)(d) EPC, to debit seven times the amount of the designation fee. If states are indicated under No. 10.2, the EPO will debit designation fees only for those states, unless instructed otherwise before the basic period expires.</p> | <p>10. Taxes de désignation</p> <p>10.1 Il est actuellement envisagé de payer un montant correspondant à sept fois la taxe de désignation. Les taxes de désignation sont ainsi réputées payées pour tous les Etats contractants de la CBE¹ désignés dans la demande internationale² (art. 2, point 3 du RRT).</p> <p>10.2 Contrairement à ce qui est indiqué au n° 10.1, il est actuellement envisagé de payer moins de sept taxes de désignation pour les Etats contractants de la CBE² suivants désignés dans la demande internationale :</p> <p>(4) <input type="text"/></p> <p>(5) <input type="text"/></p> <p>(6) <input type="text"/></p> <p>Si des Etats contractants sont mentionnés au n° 10.2, prière de ne pas procéder à la signification d'une notification prévue par la règle 108(3) CBE pour les Etats contractants n'y étant pas mentionnés.</p> <p>10.3 Si un ordre de prélèvement automatique est donné (rubrique 12), il est demandé à l'OEB de prélever, à l'expiration du délai normal visé à la règle 107(1)(d) CBE, un montant correspondant à sept fois la taxe de désignation. Si une déclaration a été faite au n° 10.2, les taxes de désignation ne sont à prélever que pour les Etats contractants qui y sont indiqués, sauf instruction contraire reçue par l'OEB avant l'expiration du délai normal.</p> |

1 Stand bei Drucklegung: 27 Vertragsstaaten, und zwar: / Status when this form was printed: 27 contracting states, namely / Situation à la date d'impression: 27 Etats contractants, à savoir : AT Österreich / Austria / Autriche, BE Belgien / Belgium / Belgique, BG Bulgarien / Bulgaria / Bulgarie, CH / U Schweiz und Lichtenstein / Switzerland and Liechtenstein / Suisse et Liechtenstein, CY Zypern / Cyprus / Chypre, CZ Tschechische Republik / Czech Republic / République tchèque, DE Deutschland / Germany / Allemagne, DK Dänemark / Denmark / Danemark, EE Estland / Estonia / Estonie, ES Spanien / Spain / Espagne, FI Finnland / Finland / Finlande, FR Frankreich / France / France, GB Vereinigtes Königreich / United Kingdom / Royaume-Uni, GR Griechenland / Greece / Grèce, HU Ungarn / Hungary / Hongrie, IE Irland / Ireland / Irlande, IT Italien / Italy / Italie, LU Luxemburg / Luxembourg / Luxembourg, MC Monaco / Monaco / Monaco, NL Niederlande / Netherlands / Pays-Bas, PT Portugal / Portugal / Portugal, RO Rumänien / Romania / Roumanie, SE Schweden / Sweden / Suède, SI Slowenien / Slovenia / Slovénie, SK Slowakische Republik / Slovak Republic / République slovaque, TR Türkei / Turkey / Turquie

2 Für folgende Staaten nur möglich, falls in der internationalen Anmeldung am oder nach folgendem Tag bestimmt: Slowakische Republik, Bulgarien, Tschechische Republik und Estland: 1. Juli 2002, Slowenien: 1. Dezember 2002, Ungarn: 1. Januar 2003 und Rumänien: 1. März 2003. / For the following states this is possible only if they are designated in the international application on or after the stated date: Slovak Republic, Bulgaria, Czech Republic and Estonia: 1 July 2002, Slovenia: 1 December 2002, Hungary: 1 January 2003 and Romania: 1 March 2003. / En ce qui concerne les Etats suivants seulement si la désignation a été effectuée dans la demande internationale à la date suivante ou à une date ultérieure: République slovaque, Bulgarie, République tchèque et Estonie: 1^{er} juillet 2002, Slovénie: 1^{er} décembre 2002, Hongrie: 1^{er} janvier 2003 et Roumanie: 1^{er} mars 2003.

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| <input checked="" type="checkbox"/> 11. Erstreckung des europäischen Patents Bei Zahlung der Erstreckungsgebühren) gilt diese Anmeldung auch als wirksamer Erstreckungsantrag für die in der internationalen Anmeldung bestimmten »Erstreckungsstaaten«. Es ist beabsichtigt, diese Gebühr(en) für folgende Staaten zu entrichten: <input type="checkbox"/> SI Slowenien ¹⁾ <input type="checkbox"/> LT Litauen <input type="checkbox"/> LV Lettland <input type="checkbox"/> AL Albanien <input type="checkbox"/> RO Rumänien ¹⁾ <input type="checkbox"/> MK Ehemalige jugoslawische Republik Mazedonien <input type="checkbox"/> _____ ²⁾ | 11. Extension of the European patent On payment of the extension fee(s) this application is also deemed to be a request for extension to all the "extension states" designated in the international application. It is intended to pay the fee(s) for the following states: Slovenia ¹⁾ Lithuania Latvia Albania Romania ¹⁾ Former Yugoslav Republic of Macedonia _____ ²⁾ | 11. Extension des effets du brevet européen La taxe (Les taxes) d'extension payée(s), la présente demande est également réputée être une demande d'extension à tous les »Etats autorisant l'extension« désignés dans la demande internationale. Il est envisagé de payer la taxe (les taxes) d'extension pour les Etats suivants: Slovénie ¹⁾ Lituanie Lettonie Albanie Roumanie ¹⁾ Ex-République yougoslave de Macédoine _____ ²⁾ |
| <p><small>1) Für Slowenien und Rumänien nur möglich, falls in der internationalen Anmeldung bis 30. November 2002 (Slowenien) oder bis 28. Februar 2003 (Rumänien) bestimmt. / For Slovenia and Romania this is possible only if they are designated in the international application up to 30 November 2002 (Slovenia) or 28 February 2003 (Romania). / En ce qui concerne la Slovénie et la Roumanie, seulement si la désignation a été effectuée dans la demande internationale jusqu'au 30 novembre 2002 (Slovénie) ou jusqu'au 28 février 2003 (Roumanie).</small></p> <p><small>2) Platz für Staaten, mit denen »Erstreckungsabkommen« nach Drucklegung dieses Formblatts in Kraft treten und die in der internationalen Anmeldung bestimmt waren. / Space for States with which "extension agreements" enter into force after this form has been printed and which were designated in the international application. / Réserve pour des Etats à l'égard desquels des »accords d'extension« entreront en vigueur après l'impression du présent formulaire et qui ont été désignés dans la demande internationale.</small></p> | | |
| <input type="checkbox"/> 12. Automatischer Abbuchungsauftrag (Nur möglich für Inhaber von beim EPA geführten laufenden Konten) Das EPA wird beauftragt, nach Maßgabe der Vorschriften über das automatische Abbuchungsverfahren fällige Gebühren und Auslagen vom untenstehenden laufenden Konto abzubuchen. In Bezug auf die Benennungsgebühren wird auf Feld 10.3 verwiesen. Das EPA wird ferner beauftragt, die Erstreckungsgebühren für jeden in Feld 11 angekreuzten »Erstreckungsstaat« bei Ablauf der Grundfrist zu ihrer Zahlung abzubuchen, sofern ihm nicht bis dahin ein anderslautender Auftrag zugeht. Nummer und Kontoinhaber | 12. Automatic debit order (for EPO deposit account holders only) The EPO is hereby authorised, under the Arrangements for the automatic debiting procedure, to debit from the deposit account below any fees and costs falling due. For designation fees, see Section 10.3. The EPO is also authorised, on expiry of the basic period for paying the extension fees, to debit those fees for each of the "extension states" marked with a cross in Section 11, unless instructed otherwise before the said period expires. Number and account holder | 12. Ordre de prélèvement automatique (uniquement possible pour les titulaires de comptes courants ouverts auprès de l'OEB) Par la présente, il est demandé à l'OEB de prélever du compte courant ci-dessous les taxes et frais venant à échéance, conformément à la réglementation relative au prélèvement automatique. Pour les taxes de désignation, se reporter à la rubrique 10.3. Il est en outre demandé à l'OEB de prélever, à l'expiration du délai normal prévu pour leur paiement, les taxes d'extension pour chaque »Etat autorisant l'extension« coché à la rubrique 11, sauf instruction contraire reçue avant l'expiration de ce délai. Numéro et titulaire du compte |
| <input checked="" type="checkbox"/> 13. Eventuelle Rückzahlungen auf das beim EPA geführte laufende Konto Nummer und Kontoinhaber | 13. Any reimbursement to EPO deposit account Number and account holder 28000200 Forrester & Boehmert | 13. Remboursements éventuels à effectuer sur le compte courant ouvert auprès de l'OEB Numéro et titulaire du compte |
| 14. Unterschrift(en) des (der) Anmelders(s) oder Vertreters Ort / Datum Für Angestellte (Art. 133(3) EPÜ) mit allgemeiner Vollmacht: Nr. Name(n) des (der) Unterzeichneten bitte in Druckschrift wiederholen. Bei juristischen Personen bitte auch die Stellung des (der) Unterzeichneten innerhalb der Gesellschaft in Druckschrift angeben. | 14. Signature(s) of applicant(s) or representative  Name: GOWSHALL JON Place / Date London, England. 17 JUNE 2005 For employees (Art. 133(3) EPC) having a general authorisation: No. Please print name(s) under signature(s). In the case of legal persons, the position of the signatory within the company should also be printed. | 14. Signature(s) du (des) demandeur(s) ou du mandataire Lieu / Date Pour les employés (art. 133(3) CBE) disposant d'un pouvoir général: N° Le ou les noms des signataires doivent être indiqués en caractères d'imprimerie. S'il s'agit d'une personne morale, la position occupée au sein de celle-ci par le ou les signataires doit également être indiquée en caractères d'imprimerie. |

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PCT/US2003/037143

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NOTIFICATION OF THE RECORDING
OF A CHANGE

(PCT Rule 92bis.1 and
Administrative Instructions, Section 422)

From the INTERNATIONAL BUREAU

To:

RYBAK, Sheree, Lynn
Klarquist Sparkman, LLP
Suite 1600
One World Trade Center
121 SW Salmon Street
Portland, OR 97204
United States of America

| | |
|--|---|
| Date of mailing (day/month/year) 18 October 2004 (18.10.2004) | IMPORTANT NOTIFICATION |
| Applicant's or agent's file reference 6395-66741 | |
| International application No. PCT/US2003/037143 | International filing date (day/month/year) 18 November 2003 (18.11.2003) |

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|---|----------------------------|--------------------------|
| 1. The following indications appeared on record concerning: <input checked="" type="checkbox"/> the applicant <input checked="" type="checkbox"/> the inventor <input type="checkbox"/> the agent <input type="checkbox"/> the common representative | | |
| Name and Address MOREY, Natalie, J. 3138 Caldwell Rd. NE Atlanta, GA 30319-2918 United States of America | State of Nationality US | State of Residence US |
| | Telephone No. | |
| | Facsimile No. | |
| | Teleprinter No. | |
| 2. The International Bureau hereby notifies the applicant that the following change has been recorded concerning: <input type="checkbox"/> the person <input type="checkbox"/> the name <input checked="" type="checkbox"/> the address <input type="checkbox"/> the nationality <input type="checkbox"/> the residence | | |
| Name and Address MOREY, Natalie, J. 2333 Ewing Dr NE Atlanta, GA 30319-3929 United States of America | State of Nationality US | State of Residence US |
| | Telephone No. | |
| | Facsimile No. | |
| | Teleprinter No. | |
| 3. Further observations, if necessary: | | |
| 4. A copy of this notification has been sent to: <input checked="" type="checkbox"/> the receiving Office <input checked="" type="checkbox"/> the designated Offices concerned <input checked="" type="checkbox"/> the International Searching Authority <input type="checkbox"/> the elected Offices concerned <input type="checkbox"/> the International Preliminary Examining Authority <input type="checkbox"/> other: | | |

| | |
|--|---|
| The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland Facsimile No. (41-22) 338.89.65 | Authorized officer Claudine PERGOD Telephone No. (41-22) 338 9207 |
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